Search Text	<b>U</b> 1
indir (ain)	integrin adj binding adj (motif or domain)
wth or	bone adj (growth or formation)
3	(1 or 2) same 3
-S.did.	wo-9514714-\$.did.
	5681353.pn.

THIS PAGE BLANK (USPTO)

Thu

```
100.0%; Score 82; DB 10; 100.0%; Pred. No. 4.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: D-00004 peptide;
NAME/KEY: AMIDATION
; LOCATION: 15
US-09-812-485A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1756
1758
1209
1209
1458
2039
2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-812-485A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-10-360-202-10
                                                                                                                                                                                                                                                                                                                                                                                                                                         49.5
49.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, App.
Seguence 10, App.
                                                                                                                                    ; Search time 21.3158 Seconds (without alignments) 146.247 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/SPCT_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                            789580
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-812-485A-47
US-10-360-202-10
US-10-360-202-9
US-10-360-202-8
US-10-360-202-8
US-10-360-202-6
US-09-812-485A-49
US-10-360-202-1
US-10-360-202-17
US-10-360-202-17
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-812-485A-1
US-09-794-422-34
US-09-814-550-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-794-422-6
US-10-311-840-1
                                                                                                                                                                                                                                                                                                                                                                                           789580 seqs, 207824079 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
                                                                                                                                      January 29, 2004, 12:38:39
                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                        1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                   US-09-812-485A-47
82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
```

ö

Gaps

ö

Length 15; Indele

```
Sequence 15, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 6, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 24, Appl
Sequence 26, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 47, Application US/09812485A

Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kunagai, Yoshinari

APPLICANT: Winagai, Yoshinari

APPLICANT: Voneda, Toshiyuki

TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases

TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases

TITLE OF INVENTION: Poptides and Methods of Treating Skeletal Diseases

TITLE OF INVENTION: Poptides and Methods of Treating Skeletal Diseases

CURRENT PILING DATE: 2001-03-19

PRIOR PILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 47

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Appli
Sequence 6, Appli
Sequence 10950, A
2 US-09-794-422-8

2 US-09-794-422-8

1 US-10-360-202-15

1 US-09-814-22-15

1 US-09-814-22-16

1 US-09-814-22-2

1 US-09-814-22-2

1 US-09-914-422-2

1 US-09-794-422-2

1 US-09-812-485A-36

1 US-09-812-485A-24

1 US-09-812-485A-25

1 US-09-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-156-761-10950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-054-691-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-192-584-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                       APPLICANT: Okano, Toshio
APPLICANT: Tsugawa, Naoko
APPLICANT: Tsugawa, Naoko
APPLICANT: Blacher, Kimie
APPLICANT: Rumagai, Yoshinari
ITILE OF INVENTION: OPVITAMIN D DEFICIENCY
ITILE OF INVENTION: OPVITAMIN D DEFICIENCY
FILE REPERENCE: BEAR-010
CURRENT APPLICATION NUMBER: US/10/360,202
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,548
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9;
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Okano, Toshio
APPLICANT: Tsugawa, Naoko
APPLICANT: Nakagawa, Kimie
APPLICANT: Blacher, Russell W
APPLICANT: Kumagal, Yoshinari
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
FITLE OF INVENTION: OF VITAMIN D DEFICIENCY
FILE REFERENCE: BEAR-010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 82; DB 12;
100.0%; Pred. No. 6.7e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82; DB 12;
Pred. No. 6.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Scorion No. V. Pred. No. V. O. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT PEDLICATION NUMBER: US/10/360,202
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,548
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Synthetic oligopeptide US-10-360-202-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic oligopeptide US-10-360-202-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10360202 Publication No. US20030186891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10360202 Publication No. US20030186891A1
Publication No. US20030186891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ERGDNDISPFSGDGQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-360-202-6
                                                                                      APPLICANT: Tengawa, Naoko
APPLICANT: Tengawa, Naoko
APPLICANT: Tengawa, Kimie
APPLICANT: Blacher, Russell W
APPLICANT: Blacher, Russell W
APPLICANT: Kumaga, Yoshinari
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF VITAMIN D DEFICIENCY
FILE REPERBNGS: BEAR-010
CURRENT APPLICATION NUMBER: US/10/360,202
CURRENT FILING DATE: 2003-02-07
PRIOR FILING DATE: 2003-02-08
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tsugawa, Naoko
APPLICANT: Nakagawa, Kimie
APPLICANT: Nakagawa, Kimie
APPLICANT: Nakagawa, Kimie
APPLICANT: Blacher, Russell W
APPLICANT: Kumagai, Yoshinari
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF VITAMIN D DEFICIENCY
TITLE OF INVENTION: OF VITAMIN D DEFICIENCY
FILE REFERENCE: BEAR-010
CURRENT APPLICATION NUMBER: US/10/360,202
FRIOM APPLICATION NUMBER: 60/335,548
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 82; DB 12;
100.0%; Pred. No. 4.9e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 82; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Synthetic oligopeptide US-10-360-202-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic oligopeptide US-10-360-202-7
Sequence 10, Application US/10360202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10360202
Publication No. US20030186891A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 9, Application US/10360202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial sequence
                       US20030186891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                         APPLICANT: Okano, Toshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Okano, Toshio APPLICANT: Tsugawa, Naok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-10-360-202-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 7
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
```

Db ò

ö

Gaps

; 0

Gaps

ò

```
Sequence 17, Application US/10360202

Sequence 17, Application US/10360202

Publication No. US20030186891A1

GENERAL INFORMATION:

APPLICANT: Okano, Toshio

APPLICANT: Nakagawa, Kimie

APPLICANT: Nakagawa, Kimie

APPLICANT: Rumagal, Yoshinari

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT

ITILE OF INVENTION: COMPOSITIONS AND METHODS

CURRENT APPLICATION NUMBER: US/10/360,202

CURRENT FILIAG DATE: 2003-02-07

PRIOR APPLICATION NUMBER: 60/335,548

PRIOR PILIAG DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 24
                                      APPLICANT: NAKAGAWA, KAMAE
APPLICANT: NAKAGAWA, KAMAE
APPLICANT: Blacher, Russell W
APPLICANT: Rumagai, Yoshinari
APPLICANT: Kumagai, Yoshinari
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF VITAMIN D DEFICIENCY
TITLE OF INVENTION: OF VITAMIN D DEFICIENCY
CURRENT APPLICATION NUMBER: US/10/360,202
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,548
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 23
SOCTIMARE: FastSEQ for Windows Version 4.0
SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 82; DB 12;
Pred. No. 7.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

100.0%; Score 82; DB 12;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic oligopeptide US-10-360-202-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic oligopeptide US-10-360-202-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-360-202-18

Sequence 18, Application US/10360202

PUDIcation No. US20030186891A1

SENERAL INFORMATION:

APPLICANT: Okano, Toshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ERGDNDISPESGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ERGDNDISPFSGDGQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
Okano, Toshio
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-360-202-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-812-465A-49
US-09-812-465A-49
US-09-812-465A-49

Sequence 49, Application US/09812485A

PUBLICACION NO. US2002197267A1

GENERAL INFORMATION:
APPLICANT: Winagai, Yoshinari
APPLICANT: Voneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Deptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT PILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 09/641,034

PRIOR PLING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 23

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                 APPLICANT: Nakagawa, Kimie
APPLICANT: Blacher, Russell W
APPLICANT: Blacher, Russell W
APPLICANT: Kumagai, Yoshinari
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF VITAMIN D DEFICIENCY
FILE REFERENCE: BEAR-010
CURRENT APPLICATION NUMBER: US/10/360,202
CURRENT APPLICATION NUMBER: 60/335,548
PRIOR PILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 82; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic oligopeptide
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: D-00006 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/10360202; Publication No. US20030186891A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S ERGDNDISPFSGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERGDNDISPFSGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ERGDNDISPESGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ERGDNDISPFSGDGQ 15
                                                Tsugawa, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: AMIDATION
LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-812-485A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-10-360-202-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-360-202-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ö

Gaps

ö

ö

Gapa

ö

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                100.0%; Score 82; DB 12;
100.0%; Pred. No. 2.3e-05;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 82; DB 10;
100.0%; Pred. No. 2.4e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09794422
Publication No. US20030166239A1
GENERAL INFORMATION:
APPLICANT: Brown, Thomas A.
APPLICANT: Gowen, Lorf C.
APPLICANT: Hames, Lynn M.
TITLE OF INVENTION: Mammalian Osteoregulins
FILE REPERBERS.
CURRENT APPLICATION WUMBER: US/09/794,422
CURRENT FILING DATE: 2001-02-27
TITLE OF INVENTION: Mammalian Osteoregulins
                               CURRENT FILING DATE: 2001-02-27
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,617
PRIOR APPLICATION NUMBER: 60/234,500
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 34
LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-814-550-2; Sequence 2, Application US/09814550; Patent No. US20020102641A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 ERGDNDISPFSGDGQ 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 ERGDNDISPFSGDGQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                  , ORGANISM: Homo sapiens
US-09-794-422-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-794-422-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-814-550-2
                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Standari, Voshinari
APPLICANT: Blandari, Russel
APPLICANT: Blandari, Russel
APPLICANT: Woneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR PILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                   APPLICANT: Nakagawa, Kimie
APPLICANT: Nakagawa, Kimie
APPLICANT: Blacher, Russell W
APPLICANT: Managai, Yoshinari
APPLICANT: Kumagai, Yoshinari
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF VITAMIN D DEFICIENCY
FILE REFERENCE: BEAR-OLD
CURRENT PELING DATE: 2003-02-07
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,548
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FRAESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 82; DB 10; Length 97; Best Local Similarity 100.0%; Pred. No. 3.8e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic oligopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: peptidic compound US-09-812-485A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34, Application US/08794422; Publication No. US20030166239A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/09812485A; Publication No. US20020197267A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Wet, Jeffrey R.
Gowen, Lori C.
Hames, Lynn M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERGDNDISPFSGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERGDNDISPFSGDGQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Brown, Thomas A. APPLICANT: De Wet, Jeffrey F. APPLICANT: Gowen, Lori C. APPLICANT: Hames, Lynn M.
      Tsugawa, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-794-422-34
                                                                                                                                                                                                                                                                                                                                                                                             US-10-360-202-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-812-485A-1
                                                                                                                                                                                                                                                                      SEQ ID NO 18
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
```

g

ò

```
ö
                                                                                                                                                   ô
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                     Length 525;
                                                                                                                            Query Match 100.0%; Score 82; DB 12; Length 525; Best Local Similarity 100.0%; Pred. No. 2.4e-05; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                  2000-09-22
   60/185,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; P. Matches 15; Conservative 0;
PRIOR APPLICATION NUMBER: 60/1
PRIOR FLING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 6
LENGTH: 525
TYPE: PRT
TYPE: PRT
TYPE: PRT
US-09-794-422-6
                                                                                                                                                                                  1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                      1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 525
; TYPE: PRT
; ORGANISM: Human
US-10-311-840-1
                                                                                                                                                                                         ద
                                                                                                                                                                       ò
```

Search completed: January 29, 2004, 12:42:43 Job time : 21.3158 secs

246 ERGDNDISPFSGDGQ 260

윱

ò

THIS PAGE BLANK (USPTO)

```
hypothetical prote
cellulase egl1 - s
arylsulfatase (EC
arylsulfatase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical prote
leucyl-tRNA synthe
brahma associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical prote hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin-like protei
En/Spm-like transp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable exported
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical prote
protein F10G7.2 [i
                                                                                                                                                                                                                                                                                                                                                                               multiple banded an lysozyme (EC 3.2.1
                                                                                                                                                                                                                                                                                                                                                                                                         probable transmemb
protein C48B4.4b [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable transcrip
                                                                                                                                                                                                                                                                                                                                                                                                 intracellular alka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable protein k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown protein [i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-keto-4-pentenoat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable hydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dihydrodipicolinat
S-adenosylmethioni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -keto-4-pentenoat
                                                                                                                                                                                                                                                                                                                                                                                                                            transport protein
                                                 January 29, 2004, 12:36:28; Search time 10.6579 Seconds (without alignments) 135.349 Million cell updates/sec
                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                  283308
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T45548
T33022
B88131
                                                                                                                                                                                                                                                                                                                                                                                                        T39285
F88559
                                                                                                                                                                                                                                                                                                                                                                                                                          S60124
AE1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F90274
F83642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C84856
B87470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S59499
B35159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A85530
F64762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B96562
                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665036
                                                                                                                                                                                                                                                                                                                                                                                                                                            D75307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G84608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H70879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483170
                                                                                                     1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                    US-09-812-485A-47
82
                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                     Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyright
                                                                                                                                                                                                                                              PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*
                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                  4444444444444444444444A444A44
                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                Score
                                 OM protein
                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                      Sequence:
                                                                                                                                                 Searched:
                                                                                                                                                                                                                                               Database
                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                   ģ
```

```
Jysozywe (EC 3.2.1.17) - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Reb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C;Accession: AD3322
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Golteman, E.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesse Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A;Reference number: AD322; PMID:1175668
A;Accession: AD3322
A;Accession: AD3322
A;Accession: AD3322
A;Accession: BDA
A;Experimental probleminary
A;Molecule type: DNA
A;References: GB:AE008917; PIDN:AAL51743.1; PID:g17982481; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                 Interstitial colla
interstitial colla
interstitial colla
stage II sporulati
                                                                                     DNA topoisomerase
DNA topoisomerase
genome polyprotein
                                                                   iron (III) dicitra
probable tumor sup
                             amidase homolog -
probable peptidase
                                                4-alpha-glucanotra
probable membrane
 protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                      Catalase
                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 913;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indele
                                                                                                                                                                                                                                                                                                                                                                                                DB 7
                                                                                                                                                                                                                                                                                                                                                                                                   54.9%; Score 45; DB
81.8%; Pred. No. 26;
ive 0; Mismatches
                                                                                                                                                                           ALIGNMENTS
           C39200
G89908
T29430
D96017
                                               A45049
S65196
F71894
JN0598
JS0703
JS0703
KCHUI
KCHUI
KCHOI
S66094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        891 NDISPFSKDDQ 901
  402
416
507
507
612
612
792
11166
793
8273
8273
8273
                                                                                                                                                                                                                                                                                                                                                                                                                                         5 NDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: BMEI0562
                                                                                                                 38.5
38.5
38.5
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
AD3322
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                            유
```

53.7%; Score 44; DB 2; Length 277;

Query Match

(1

```
Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENESNDSTPLRGDGO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 ENESNDSTPLRGDGQ 56
                                                                                                                 A; Accession: F88559
A; Status: preliminary
                                                                                                                                                                                                                                                              A; Map position: 3
                                                                                                                                                                                                                                          C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                intracellular alkaline serine proteinase aprX [imported] - Bacillus halodurans (strain C). Species: Bacillus halodurans
C, Species: Bacillus halodurans
C, Date: 0.1 Dec. 2000 #sequence_revision 0.1 Dec. 2000 #text_change 15 Jun-2001
C, Accession: B83891
R, Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A, Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A, Reference number: A83650; MUID: 20512582; PMID: 11058132
A, Accession: B83891
A, Molecule type: DNA
A, Residues: 1-444 <STO>
A, Residues: 1-444 <STO>
A, Residues: 1-444 <STO>
A, Experimental source: strain C-125
C, Genetics: A, Gene: aprX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transmembrane protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C;Accession: T39285
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Bothe, G.; Pohl, T. submitted to the EMBL Data Library, July 1999
A;Reference number: Z21841
A;Accession: T39285
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Katus: preliminary; translated from GB/EMBL/DDBJ
A;Katus: DNA
A;Residues: 1-629 <MCD>
A;Cross-references: EMBL:AL096851; PIDN:CABS0971.1; GSPDB:GN00067; SPDB:SPBC1105.08
A;Experimental source: strain 972h-; cosmid c1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: SPDB:SPBC1105.08
A;Map position: 2
A;Introns: 67/1
C;Superfamily: Schizosaccharomyces pombe probable transmembrane protein SPBC1105.08
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein C48B4.4b [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C;Accession: F88559
R;anonymous, The C. elegans Sequencing Consortium.
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.4%; Score 43; DB 2; Length 444; 50.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 2; Length 629;
Pred. No. 37;
1; Mismatches 2; Indels
                        Indels
                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 25;
4; Mismatches
Pred. No. 10;
2; Mismatches
                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.4%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ERGDNDISPFSGDG 14
                                                                                                                    252 RGDADINTFAGD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.7.
Best Local Similarity 72.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.4
Best Local Similarity 50.0
Matches 7; Conservative
Best Local Similarity 66.7
Matches 8; Conservative
                                                                       2 RGDNDISPFSGD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 NDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTISPFIGDGR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Genetics:
                                                                       ð
                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
A,Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A,Reference number: A75000; MUID:99069613; PMID:9851916
A,Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Map position: III
A introns. 47/1; 112/3; 161/2; 220/2; 543/3; 574/3; 903/2; 1056/1; 1115/3; 1178/3; 1265/;
A introns. 47/1; 112/3; 161/2; 220/2; 543/3; 574/3; 903/2; 1056/1; 1115/3; 1178/3; 1265/;
C Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology cassette bromology cassette br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mypothetical protein al10406 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. pCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Accession: AE1857
C;Accession: AE1857
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. NAttle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1857
A;Accession: AE1857
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1758 <STO>
A;Cross-references: GB:chr_III; PIDN:CAA82384.1; PID:g3875025; GSPDB:GN00021; CESP:C48B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transport protein homolog C48B4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: S60124; S40724; S40725
R;Kershaw, J.
Submitted to the EMBL Data Library, November 1995
A;Reference number: S60124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 2; Length 1767;
Pred. No. 1.1e+02;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.4%; Score 43; DB 2; Length 1758; Best Local Similarity 53.3%; Pred. No. 1.1e+02; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1767 <KER>
A;Cross-references: EMBL:Z29117; NID:g439247; PID:g1066912
```

2; Mismatches

Query Match Best Local Similarity 70.0 Matches 7; Conservative

ઠે a

```
Nypothetical protein YKR088c - yeast (Saccharomyces cerevisiae)

NyAlternate names: hypothetical protein YKR408
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision
C;Accession: S38166; S42017; S39129
R;Baladaron, V; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Bsteban, P.F.; Garcia-Cantalejo, A;Reference number: S38158
A;Reference number: S381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast 10, 231-245, 1994
A/Title: The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae chromk A/Reference number: S42009; MUID:94262327; PMID:8203164
A/Rocession: S42017
A/Molecule type: DNA
A/Rocidues: 1-337 <GAR>
A/Cross-references: EMBL:227116; NID:g415899; PIDN:CAA81639.1; PID:g415908
C/Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: G65036

K; Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID: 97426617; PMID: 9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-886 < MLAT-
A;Cross-references: GB:Ab000344; GB:U00096; NID:g1788927; PIDN:AAC75637.1; PID:g1788938;
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Escherichia coli
C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 2; Length 337;
Pred. No. 41;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 41; DB 2; Length 886; 70.0%; Pred. No. 1.1e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein b2584 - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;96-112/Domain: transmembrane #status predicted <TM1>F;138-154/Domain: transmembrane #status predicted <TM2>F;134-190/Domain: transmembrane #status predicted <TM3>F;290-306/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: SGD:S0001796
A,Map position: 11R
C;Keywords: transmembrane protein
F;96-112/Domain: renewant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 DNDIMPNSNNGO 39
                                       380 RCDNDMMPIKG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 DNDISPESGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  693 DISPFECTONE 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 DISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leucyl-tRNA synthetase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75307
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathwan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T13153
R;Papoulas, O.; Beek, S.J.; Moseley, S.L.; McCallum, C.M.; Sarte, M.; Shearn, A.; Tamkun R;Papoulas, O.; Beek, S.J.; Moseley, S.L.; McCallum, C.M.; Sarte, M.; Shearn, A.; Tamkun B;Papoulas, O.; 3955-3966, 1998
A;Title: The Drosophila trithorax group proteins BRM, ASH1 and ASH2 are subunits of dist A;Reference number: 217610; MUID:98407952; PMID:9735357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-874 «WHI>
A;Cross-references: GB:AE002050; GB:AE000513; NID:g6459965; PIDN:AAF11720.1; PID:g645997
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
A;Residues: 1-420 <KUR>
A;Residues: 1-420 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72364.1; PID:g17129751; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF071502; NID:g3378131; PID:g3378132; PIDN:AAC28454.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gарв
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
T13153
brahma associated protein 155K - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2; Length 1209;
Pred. No. 1.18+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 874;
                                                                                                                                                                                                                                                        51.2%; Score 42; DB 2; Length 420; 70.0%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Description: anactivator of Drosophila homeotic genes
```

DB 2; 77;

51.2%;

Best Local Similarity 53.8 Matches 7, Conservative

Query Match

A;Map position: 1 C;Superfamily: leucine-tRNA ligase

2; Mismatches Score 42; Pred. No. 7

> > 셤

ò

51.2%;

Best Local Similarity 63.6 Matches 7; Conservative

Query Match

A,Accession: T13153 A,Status: preliminary: translated from GB/EMBL/DDBJ A,Molecule type: mRNA A,Residues: 1-1209 <PAP>

A; Cross-references: FlyBase: FBgn0002783

A, Map position: 3 C, Function:

A; Accession: AF0772

```
Search completed: January 29, 2004, 12:40:56 Job time : 11.6579 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 RGDNDAIVAVWAGDG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: F90274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       En/Spm-like transposon protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: G84608
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84608
A;Status: praliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
AF0772
AF0772
Probable exported protein STY2350 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cjaccession: AF0772
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
Ajathors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Ajritle: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE002093; NID:g4587588; PIDN:AAD25816.1; GSPDB:GN00139 C;Genetics:
myosin-like protein ATM - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Dacies: Arabidopsis thaliana (mouse-ear cress) C;Dacession: 333812 R;Knight, A.E.; Kendrick-Jones, J. J. Mol. Biol. 231, 148-154, 1993 A;Title A myosin-like protein From a higher plant. A;Reference number: S33812; MUID:93267647; PMID:7684453
                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1166 <KNI>
A;Cross-references: EMBL:X69505; NID:g297068; PIDN:CAB61875.1; PID:g6491702
C;Superfamily: myosin heavy chain 95F; myosin motor domain homology
C;Superfamily: myosin binding; coiled coil; nucleotide binding; P-loop
F;168-825/Domain: myosin motor domain homology <MMOT>
F;168-825/Domain: myosin motor domain homology <MMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.8%; Score 40; DB 2; Length 140; 57.1%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 2; Length 116
Pred. No. 1.5e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAGDNDDEPEGDDG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ERGDNDISPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GDSEDSPYSGHG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GDNDISPFSGDG 14
                                                                                                                                                                                                                                                          A; Accession: S33812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: At2g22080
A,Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
```

```
hypothetical protein porB-1 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accesion: F90274
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Vong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Parmett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                    ö
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02500.1; PID:g16503364; GSPDB:GN00176
C;Genetics:
A;Gene: STY2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <KUR>
A;Cross-references: GB:AE006641; NID:g13814401; PIDN:AAK41453.1; GSPDB:GN00155
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 300;
                                                                                                                                           Length 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
53;
                                                                                                                                           Score 40; DB 2;
Pred. No. 41;
                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Genetics:
A;Gene: porB-1
C;Superfamily: pyruvate synthase beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.8%;
53.3%;
                                                                                                                                         Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RGDND--ISPFSGDG 14
                                                                                                                                                                                                                                                      :|:::||: |||
90 KGESFLSPYIGDG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.3%
                                                                                                                                                                                                                            2 RGDNDISPFSGDG 14
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

January 29, 2004, 12:35:18; Search time 8.28947 Seconds (without alignments) 85.096 Million cell updates/sec Run on:

US-09-812-485A-47 82 1 ERGDNDISPFSGDGQ 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ge :	P36164 saccharomyc									Q06801 solanum tub		_			P25927 salmonella	P16342 murine coro	P28053 bos taurus	Q9xsz5 equus cabal	hod	Bug					-	Q42463 lycopersico		mus m	Q8wyr4 homo sapien	strep		Q13336 homo sapien
SUMMARIES	ID	SYL DEIRA	YK68 YEAST	YFIQ_ECOLI	RUXX THEAC	GUN1_USTMA	ARS KLEAE	MHPD ECOLI		QUEA PSEAE	U120 HSVMG	DPEP_SOLTU	YP68_YEAST	L2GL_DROPS	TP2A_RAT	TP2A MOUSE	BIGA SALTY	RRPB_CVMAS		MMO1 HORSE			SP2E_BACSU				ATA1_MAKNI		PORI RHOCA		TSA2_HUMAN	IPNS_STRJU		UT1_HUMAN
	DB	_	-	-	٦	٦	Н	-	-	-	-	Н	-	-	-	-	-	н	Н	-	-	-1	-	-	ч	-	-	Н	-	-	-	-	Н	-
d	Length		337	986	83	393	464	569	300	347	402	576	612	1166	1526	1528	1953	2733	469	469	469	469	827	263	621	684	966	224	301	301	309	329	352	389
	Query Match	1.2	0	50.0	48.8	48.8	48.8	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.0	47.0	47.0	47.0	47.0	٠	46.3	٠	٠	٠	45.1	45.1	45.1	45.1	45.1	45.1
	Score	42	41	41	40	40	40	39	39	39	39	39	39	39	39	39	39	m	₩.	38.5	а	Θ.	8	38	38	38	38	37	37	37	37	37	37	37
	Result No.	;	7	m		'n	9	7	œ	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	53	30	31	32	33

P12851 actinoplane P24719 saccharomyc P51022 drosophila P7863 cahirosacch Q0741 papio cynoc P3466 caenorhabdi P32486 saccharomyc P51134 saccharomyc P5107 mus musculu P3350 saccharomyc P36004 saccharomyc P648437 mus musculu
XYLA ACTMI MEKL YEAST PNT1_DROME SKR1 SCHPO ITBS_PAPCY YOL2_CAEEL KRE YEAST KKQB YEAST FKXQB YEAST PRX1_MOUSE SKN1_YEAST ITBS_MOUSE
алалалалала
39 4893 4893 7720 7737 7737 7737 7737
₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩

## ALIGNMENTS

```
Nature 407:508-513(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=DSM 1728;
                                                            NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acidophilum."
                                                                                                                                                                                                                                                                                                                                      STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _RUXX_THE
P57670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RUXX_THEAC
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94262327; PubMed=8203164; Garcia-Cantalejo J., Baladron V., Esteban P.F., Santos M.A., Bou G., Garcia-Cantalejo J., Balladron V., Esteban P.F., Jimenez A., del Rey F.; Remacha M.A., Revuelta J.L., Ballesta J.P.G., Jimenez A., del Rey F.; "The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae chromosome XI contains the HBSI, MRP-L20 and PRP16 genes, and sarx new open reading frames.";
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                               ;
0
                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 38.3 kDa protein in PRP16-SRP40 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 337;
Pred. No. 14;
1; Mismatches 3; Indels
                   Score 42; DB 1; Length 823;
Pred. No. 25;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7EA95DD4E5AF77FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFIQ_ECOLI

D_YFIQ ECOLI

AC P76594 Q47120;

DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 35, Last sequence update)

DF 16-OCT-2001 (Rel. 40, Last annotation update)

DF Hypochetical protein yfiQ.
                                                                                                                                                                                                                                                     337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
S POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                 51.2%; Scotilarity 53.8%; Pre
Conservative 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38311 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z27116; CAA81639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA82167.1; -.
                                                                                                                              3 GDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 66.7
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNDIMPNSNNGQ 39
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246
271
309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S38166; S38166.
SGD; S0001796; YKR088C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein;
TRANSMEM 96 115
  Ouery Match
Best Local Similarity
7, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 2
287 3
337 AA;
                                                                                                                                                                                                                                                                                                                                                                               YKR088C OR YKR408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z28313;
                                                                                                                                                                                                                             YK68 YEAST
AC P36164;
DT YK68 YEAST
AC 01-JUN-1994
DT 01-JUN-1994
DE HYPOCHETICAL
GN SACCHAROMYCE
OC BUKARYOCA; FRO
RE BUKARYOCA; FRO
RA GARCIA-CANTA
RA REDCINE-9426
RA GARCIA-CANTA
RA REDCINE-9426
RA GARCIA-CANTA
RA REBCINE-9426
RA GARCIA-CANTA
RA REBCINE-9426
RA GARCIA-CANTA
RA REBCINE-9426
RA GARCIA-CANTA
RA REBCINE-10-231
CC This SWISS-PC
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                         엄
                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruepp A., Graml W., Santos-Marrinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                               STRAIN=K12 / MG1655;
MEDLINE=97426617; Plubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nashimoto H., Saito N.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, IN THE N-TERMINAL, TO SUCCINYL-COA LIGASES.
-!- SIMILARITY: STRONG, TO M.JANNASCHII MJ0590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmatacae; Thermoplasma.
VCBL_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 41; DB 1; Length 886; 70.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255944B9E2961251 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BNBL; D04044, D04044, D04046, G65036, G740, G740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000344; AAC75637.1; -. EMBL; D64044; BAA10925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative snRNP Sm-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886 AA; 97987 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-612 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                693 DISPFECTIVE 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 DISPFSGDGQ 15
                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
```

ö

```
ARS KLEAE
P20713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 7
                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                  RESULT 6
ARS_KLEAE
 STTTTTTS
                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOL. CHEM. HOPPE-SOYIET 376:617-625(1995).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4 beta-D-glucosidic
linkages in cellulose, lichemin and cereal beta-D-glucans.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: HYPHAL TIP.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN FILAMENTOUS DIKARYON.
-!- PTM: MAY ALSO BE O-GLUCOSYLATED.
-!- PTM: MAY ALSO BE O-GLUCOSYLATED.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96145728; PubMed=8590631;
Schauwecker F., Wanner G., Kahmann R.;
"Filament-specific expression of a cellulase gene in the dimorphic
fungus Ustilago maydis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
Endoglucanase 1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 1)
(Cellulase 1) (EG 1)
                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
                                                                                                                                                                                                                        SMART; SM00651; Sm; 1.
Hypothetical protein; Ribonucleoprotein; Complete proteome.
SEQUENCE 83 AA; 9070 MW; 07D132A75150864D CRC64;
                                                                                                                                                                                                                                                                               Score 40; DB 1; Length 83;
Pred. No. 4.2;
0; Mismatches 3; Indels
-1- SIMILARITY: Belongs to the snRNP Sm proteins family.
                                                                                                                                                                                                                                                                                                                                                                                                                                        393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000334; Glyco hydro 45.
Pfam; PF02015; Glyco hydro 45; 1.
                                                                                                                                  EMBL, AL445067; CAC12364.1; --
HAMAP; MF 00257; -; 1.
InterPro; IPR006649; BNRNP.
InterPro; IPR001163; BNRNP_Sm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ustilago maydis (Smut fungus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S81598; AAB36147.1; -.
                                                                                                                                                                                                                                                                                 48.84;
                                                                                                                                                                                            Pfam; PF01423; Sm; 1.
ProDom; PD020287; snRNP; 1.
                                                                                                                                                                                                                                                                                                                                     2 RGDNDI -- SPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                              68 RGDNVIFVSPSKGDG 82
                                                                                                                                                                                                                                                                                            Local Similarity 66.7 es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S59499; S59499.
HSSP; P43316; ZENG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-FBD11;
                                                                                                                                                                                                                                                                                                                                                                                                                                        USTMA
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
GUN1_USTMA
                                                                                                                                                                                                                                                                                                            Matches
ઠ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A sulfur- and tyramine-regulated Klebsiella aerogenes operon containing the arylaulfatase (atsA) gene and the atsB gene.";
J. Bacteriol. 172:2131-2140(1990).
-!- FUNCTION: AS IS COMMONLY PRODUCED BY SOIL MICROORGANISMS AND PLAYS AN IMPORTANT ROLE IN THE MIRREALIZATION OF SULFATES.
-!- CATALYTIC ACTIVITY: A phenol sulfate + H(2)0 = a phenol + sulfate.
-!- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Glycoprotein.
SIGNAL 1 26 POTENTIAL.
27 393 ENDOGLUCANASE 1.
ACT_GITE 152 PROTON DONOR (BY SIMILARITY).
ACT_GITE 152 PROTON DONOR (BY SIMILARITY).
ACT_GITE 270 385 ALA/GLY/SER-RICH.
CARBOHYD 343 N-LINKED (GLCANAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-077-1996 (Rel. 34, Last annotation update)
Arylsulfatase precursor (EC 3.1.6.1) (Aryl-sulfate sulphohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murooka Y., Ishibashi K., Yasumoto M., Sasaki M., Sugino H.,
Azakami H., Yamashita M.;
                                                                          ENDOGLUCANASE 1.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
ALA/GLY/SER-RICH.
N-LINKED (GLCNAC. . ) (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 464;
                                                                                                                                                                                                                                                             DB 1; Length 393;
24;
                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 ARYLSULFATASE.
134 POTENTIAL.
51471 MW; C8D09AB9EEF9C627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AA
                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 21-33.
MEDLINE=90202736; PubMed=2180918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00884; Sulfatase; 1.
PROSITE; PS00523; SULFATASE 1; 1.
PROSITE; PS00149; SULFATASE_2; 1.
Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulfatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gamma
Enterobacteriaceae, Klebsiella.
                                                                                                                                                                                                             39594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M31938; AAA25051.1; -.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ERGDNDISPFSGD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | :||||| |:
35 DMGYSDISPFGGE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     237 KDDNTISPYSG 247
                                                                                                                                                                                                                                                                                                                                                                  2 RGDNDISPFSG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella aerogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR000917;
                                                                                                                             152 1
270 3
343 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B35159; B35159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=28451;
```

```
269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                   DAPA MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bishai W.;
                 SEQUENCE
CONFLICT
                                                                                                                                                                                                                                                                                    033295;
                                                                                                                                                                                                                           RESULT 8
DAPA MYCTU
                                                                                                                                   8
                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                     MHPD_ECOLI STANDARD, PRT, 269 AA.
P77608; P71205; P77045;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-keto-4-pentenoate hydratase (EC 4.2.1.-) (2-hydroxypentadienoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12 / MGI655,
Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
Edderspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
Namach A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Purification, characterisation and reaction mechanism of monofunctional 2-hydroxypentadienoic acid hydratase from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 251:98-106(1998).

-!- COFACTOR: Requires a divalent metal ion for activity, optimum activity is obtained with Mn(2+).

-!- ENZYME REGULATION: Inhibited by sodium oxalate.

-!- PATHWAY: 3 - hydroxyphenylpropionate degradation.

-!- PATHWAY: 3 - hydroxyphenylpropionate degradation.

-!- SIMILARITY: BELONGS TO THE TODJ/XXLJ/HPCG FAMILY.
                                                                                                                                                                                                            Bscherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpró, IPR002607, Hyratase decarb.
Pámi, PF01689; Hyratase decarb; 1.
Probom; PD003731. Hyratase decarb; 1.
Aromatic hydrocarbons catabolism; Lyase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ferrandez A., Garcia J.L., Diaz E.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D86239; BAA13055.1; -. EMBL; Y09555; CAA70750.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98151237; PubMed=9492273;
                                                                                                                                                                                                                                                   Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000142; AAC73453.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U73857; AAB18074.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pollard J.R., Bugg T.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EcoGene; EG14274; mhpD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=K12 / CS520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-6,
                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                            MHPD OR B0350.
                                                                                                                                                                                                                                                                                                                                               Kawamukai M.;
                                                                                                                                                                                                                                                                                                                              STRAIN=K12
                                                                                                                                                                          hydratase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli.";
                   RESULT 7
MHPD_ECOLI
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland S., Gwinn M.L., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dihydrodipicolinate + 2 H(2)O.
-!- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate
semialdehyde; first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.T., Brosch R., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Ollver S., Osborne J., Quall M.A., Rajandraem M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Complete genome sequence:

Nature 393:537-544 (1998).
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-aspartate 4-semialdehyde + pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                           DB 1; Length 269;
                                                                                                     1; Indels
202 G -> E (IN REF. 1).
28890 MW; 34A81A8A4E236358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the DHDPS family.
                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dihydrodicicolinate synthase (EC 4.2.1.52) (DHDPS).
DAPA OR RV2753C OR MT2823 OR MTV002.18C.
                                                                                                     1; Mismatches
                                                         Score 39; DB
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL008967; CAA15549.1; -. EMBL; AE007110; AAK47142.1; -.
                                                             47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                           Query Match 47.6
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; H70879; H70879.
HSSP; P05640; 1DHP.
TIGR; MT2823; -.
TubercuList; Rv2753c;
                                                                                                                                            3 GDNDISPFS 11
                                                                                                                                                                     89 GDNEIIPFS 97
```

```
347 AA; 38160 MW; 48ECBF074C2BC589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                              U120 HSVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirai K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT SITE
SEQUENCE
    SEQUENCE
                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                 RESULT 10
U120_HSVMG
                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                            Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-denosylmethionine: RNA ribosylrransferase-isomerase (EC 5.-.-.)
(Queuosine biosynthesis protein queah).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenosylmethionine-requiring step. The ribosyl moiety of AdoMet transferred and isomerized to the epoxycyclopentane residue of (By similarity).

-I- PATHWAY: Queuosine biosynthesis.
-I- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMÁÞ; MF_00113; -; 1.
InterPro; IPR003699; Queuosine_synth.
Jemi; PF02547; Queuosine_synth; 1.
TIGRPAMs; TIGR00113; QueA; 1.
Queuosine biosynthesis; Transferase; Isomerase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                              47.6%; Score 39; DB 1; Length 300; 75.0%; Pred. No. 26; tive 2; Mismatches 0; Indels
                                                                                      PRINTS; PROO146; DHPICSNTHASE.
ProDom; PD001859; DHDPS; 1.
TIGRFAME; TICRO0674; dapp; 1.
PROSITE; PSO0665; DHDPS 1; 1.
PROSITE; PSO0666; DHDPS 2; 1.
Lyase; Diaminopimelate Biosynthesis; Lysine biosynthesis;
                                                                                                                                                                                                                                                 BY SIMILARITY.
71CB322661416367 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE004799; AAG07211.1; -.
                                                                                                                                                                                                                                               171 171 B
300 AA; 30858 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
HAMAP, MP_00418; -; 1.
InterPro; IPR005263; DapA.
InterPro; IPR002220; DHDPS.
Pfam; PF00701; DHDPS; 1.
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.v
Best Local Similarity 75.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         7 ISPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                ::||||||
20 VTPFSGDG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A83170; A83170.
                                                                                                                                                                                                                          Complete proteome.
ACT SITE 171
SEQUENCE 300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUEA OR PA3824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUEA PSEAE
Q9HXH8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
QUEA_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAN TO THE TOUR TO THE TOUR TO THE TOUR TO THE TOUR THE T
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence determination and genetic content of an 8.9-kb restriction fragment in the short unique region and the internal inverted repeat of Marek's disease virus type 1 DNA."; virus Genes 6:365-378(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDV-specific genes.";
Virology 206:324-338(1995)
-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-93118245; PubMed=1282282;
Sakaguchi M., Urakawa T., Hirayama Y., Miki N., Yamamoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95131166; PubMed-7831788; Brunovskie P., Velicer L.F.; "The Marek's disease virus (MDV) unique short region: alphaherpesvirus-homologous, fowlpox virus-homologous, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probom; PD000001; Prot Kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; PALSE_NEG.
PROSITE; PS00109; PROTEIN KINASE_ST; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
Transferase; Serine/threomine-protein kinase; ATP-binding.
Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 402;
                                                        Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93E29494B3572C7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Marek's disease-like viruses.
NCBI_TaxID=10388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marek's disease herpesvirus (strain GA) (MDHV).
  DB 1;
                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
USI206 OR US3.
                                                                                                                                                                                                                                                                                                   402 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 36;
1; Mismatches
                                                        2; Mismatches
                            Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.6%; Score 39; 50.0%; Pred. No.
  Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M80595; AAB59895.1; -.
EMBL; L22174; AAA64965.1; -.
INTEXPRO; IPR000719; Proct kinase.
InterPro; IPR002290; Ser Lhr_pkinase.
Pfam; PF00069; pkinase; I.
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44715 MW;
  47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ERGDNDISPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 50.0 nes 7; Conservative
                                                        6; Conservative
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                 263 DGELKPPSGD 272
                                                                                                              4 DNDISPFSGD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 AA;
                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
```

69 ESQSEDLSPFGNDG 82

유

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib>sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 53-57; 174-183 AND 247-259.

STRAIN=cv. May Queen; TISSUB=Tuber;
MEDLINE=9312326; bubMed=6 5.8. Smith S.M.;
Takaha T. Yanase M., Okada S., Smith S.M.;
Takaha T. Yanase M., Okada S., Smith S.M.;

"Disproportionating enzyme (4-alpha-glucanotransferase; EC 2.4.1.25)
of potato. Purification, molecular cloning, and potential role in starch metabolism.";

J. Biol. Chem. 268:1391-1396(1993).

C. I- FUNCTION: MAY ACT DURING STARCH BREAKDOWN TO CONVERT SMALL OLIGOSACCHARIDES INTO LARGER MOLECULES UPON WHICH STARCH PHOSPHORYLASE CAN ACT, OR MAY CHANGE THE STRUCTURE OF STARCH MOLECULES AND GRAIN ARCHITECTURE BY MODIFYING CHAIN LENGTH, OR MAY GENERATE FROM STARCH AND GLUCOSE OLICOSACCHARIDES WHICH CAN SERVE EITHER AS PRIMERS FOO NEW STARCH PHOSPHOENZYME.

C. I- CATALYTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan to a new 4-position in an acceptor, which may be glucose or (1,4)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: PRESENT IN LEAVES, STEMS, ROOTS, AND STOLONS BUT IS MOST ABUNDANT IN DEVELOPING AND MATURE TUBERS. SIMILARITY: BELONGS TO THE DISPROPORTIONATING ENZYME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                             Solanum tuberosum (Potato).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                           01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
4-alpha-glucanotransferase, chloroplast precursor (EC 2.4.1.25)
(Amylomalease) (Disproportionating enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003385; Glyco hydro 77.

Pfam; PF02446; 4A glucanotrans; I.

TIGREAMs; TIGR00217; mal0; 1.

Transferase; Glycosyltransferase; Carbohydrate metabolism;
Amyloplast; Chloroplast; Transit peptide.

TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.6%; Score 39; DB 1; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           576 4-ALPHA-GLUCANOTRANSFERASE.
64950 MW; AOD16F3A546307BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: CHLOROPLAST OR AMYLOPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 612 AA.
576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 54;
3; Mismatches
                                      01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X68664; CAA48630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||: | ||:||
KRGNEDGSPYSG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 58.3
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ERGDNDISPFSG 12
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A45049; A45049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 5
576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     087172; 1CWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
YP68_YEAST
ID _YP68_YEAST
DPEP SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
    ò
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STATIS-25866 / AB972;

MEDLINE-97313271; PubMed-9169875;

Bussey H., Storme R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Churcher C.M., Coster F., Davis K., Davis R.W., Ductach F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U., Heumann K., Johnston M., Kalman S., Kleine K., Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., A Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., A Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., A Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., A Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Woestl D., A Scherens B., Schramm S., Schrader M., Schrafe M., Schrafe M., Schrafe M., Schrafer M., Schrafe M., Schrafe M., Schram S., Wandy Y., Wedler E., Wedler H., Winnett E., Walber S., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Mals S., Wos M., Wals S., Wos M., Wals S., Wolliner A., Vo D.H., Hani J.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

"Atture 387.103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modulated and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBb outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 68.7 kDa protein in PPQ1-MFAL1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ALA.
A1B2EB381C0BBC8E CRC64;
                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | FILE | PROBLE | PROBLE | PROBLE | PROBLE | PROBLE | PROBLE | PROSITE; PSCOLO2; RRM; 4. | PROSITE; PSCOLO2; RRM RNP 1; 1. | RNA-BINDING (RRM) 1. | PROPERTY | PROPERTY | PROBLE | PROB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.2.E.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 1
Pred. No. 58;
3; Mismatches
                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z73540; CAA97894.1; -.
PIR; S65196; S65196.
SGD; S0006105; YPL184C.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 4.
SMART; SM00360; RRM; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68663 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || |::||| :
144 ERSSNEVSPFDDE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ERGDNDISPFSGD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274
379
504
602
19
28
419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      612 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
ò
```

RESULT 13 L2GL\_DROPS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003594; ATPbind ATPase.

R InterPro; IPR003597; CBFA NFYB topis.

R InterPro; IPR003597; CBFA NFYB topis.

R InterPro; IPR003205; DNA_CopoisoII.

R InterPro; IPR002205; DNA_CopoisoIV.

R InterPro; IPR002205; DNA_CopoisoIV.

R Pfam; PF00218; HATPase c; 1.

R PRINTS; PR00418; TP12PAMILY.

R PRINTS; PR00418; TP12PAMILY.

R PRINTS; PR00418; TP12PAMILY.

R RAART; SM0033; TOP2c; 1.

R SWART; SM0043; TOP2c; 1.

R SWART; SM0043; TOP2c; 1.

R RAART; SM0043; TOP2c; 1.

R ROSTIE; PS00177; TOPOISOWERASE II; 1.

R PROSTIE; PS00177; TOPOISOWERASE II; 1.

R PROSTIE; PS01177; TOPOISOWERASE II; 1.

R PATP (POTENTIAL).

R PATP (POTENTIAL).
                                                                                                                                                  Biochem Biophys. Res. Commun. 193:787-793(1993).
-!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS.
                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                     STRAIN=Sprague-Dawley; TISSUE=Testis;
MEDLINE=93290677; PubMed=839053;
Park S.H., Yoon J.H., Kwon Y.D., Park S.D.;
"Nucleotide sequence analysis of the CDNA for rat DNA topoisomerase
                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Homodimer.
-!- SUBCELLUAR LOCATION: Nuclear.
-!- MISCELLANEOUS: EUKARYOTIC TOPDISOMERASE I AND II CAN RELAX BOTH
-!- MISCELLANEOUS: EUKARYOTIC TOPDISOMERASE PROKARYOTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: Belongs to the type II topoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.6%; Score 39; DB 1; Length 152
54.5%; Pred. No. 1.6e+02;
tive 3; Mismatches 2; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TP2A MOUSE STANDARD; PRT; 1528 AA. 001320; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) DNA topoisomerase II, alpha isozyme (EC 5.99.1.3). TOP2A OR TOP2 OR TOP-2. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                RELAX ONLY NEGATIVE SUPERCOILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, Z46372; CAA86496.1; -.
EMBL, Z19552.CAA79611.1; -.
EMBL, Z29676; -; NOT_ANNOTATED_CDS.
HSSP, P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 54.5
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 GDMELKPFSGE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GDNDISPFSGD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090 [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
TP2A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOLLICLE CELLS.

DEVELOPMENTAL STAGE: EXPRESSED ABUNDANTLY IN EARLY EMBRYOGENESIS.

MODERATE EXPRESSION IS FOUND IN LARVAL AND ADULT STAGES.

DISEASE: MUTATIONS IN L(2) GL CAUSE MALIGNANT TRANSPORMATION OF THE OPTIC CENTRES OF THE LARVAL BRAIN AND THE IMAGINAL DISCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Buthoria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: EXPRESSED IN THE EPITHELIAL CELLS OF THE DIGESTIVE TRACT AND IN GONADS, IN THE OVARY'S NURSE AND OOCYTE'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                               Drosophila pseudoobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7237;
                                                                                                                                                                                                                                                                                                                                                                                                                                              The 1(2)gl homologue of Drosophila pseudoobscura suppresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: CELLULAR MEMBRANE OR INTERCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.6%; Score 39; DB 1; Length 1166; 58.3%; Pred. No. 1.2e+02; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93275648; PubMed-8389031;
Toeroek I., Hartenstein K., Kalmes A., Schmitt R., Strand
Mechler B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 539 1.
615 629 2.
1166 AA, 127216 MW, 8155B8AB45BD6AC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumorigenicity in transgenic Drosophila melanogaster.
Oncogene 8:1537-1549(1993).
--- FUNCTION: COULD ACT AS TUMOR SUPPRESSOR.
--- SUBUNIT: MAY FORM MULTIMERIC COMPLEXES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TP2A RAT
TP2A RAT
TP2A RAT
TP2A RAT
AC P41516,
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).
GN TOP2A OR TOP2 OR TOP2.
                                                01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-EEB-1996 (Rel. 33, Last annotation update)
Lethal(2) giant larvae protein (P127).
  PRT; 1166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X73259; CAA51715.1; -.
PIR, S37692; S37692.
FlyBase; FBQ00012725; Dpse\l(2)gl.
InterPro; IPRO00664; Lethal2 giant.
PRINTS; PRO0962; LETHAL2GIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| ||: |||
286 QRGTNDVIVFSG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 58.3
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ERGDNDISPFSG 12
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-oncogene; Repeat
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
L2GL DROPS
Q08470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

SO THE REAL PROPERTY OF THE PR

REPEAT REPEAT

Matches

ò

SXCOOS BELLIACE

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                       McPherson J., Brown G.A., Goldenberg G.J.;

"Characterization of a DNA topolsomerase Italpha gene rearrangement in adriamycin-resistant P388 leukemia: expression of a fusion messenger RNA transcript encoding topolsomerase Italpha and the retinoic acid receptor alpha locus.";

Cancer Res. 53.5885-5889(1993).

-! FUNCTION: COMPROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE IN MARES DOUBLE-STRAND BREAKS.

-! CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPARATION OF THE STATE OF STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear.
MISCELLULAR LOCATION: ULCLAR TOPOISOMERASE I AND II CAN RELAX BOTH
MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES.
RELAX ONLY NEGATIVE SUPERCOILS.
SIMILARITY: Belongs to the type II topoisomerase family.
                                                             Adachi N., Miyaike M., Ikeda H., Kikuchi A.;
Characterization of cDNA encoding the mouse DNA topoisomerase II
that can complement the budding yeast top2 mutation.";
Nucleic Acids Res. 20:5297-5303(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 1; Length 1528;
Pred. No. 1.6e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00204; DNA_topoisolV.
Ffam; PF00204; DNA_gyraseB; 1.
Ffam; PF00521; DNA_topoisolV; 1.
Ffam; PF00518; HATPase c; 1.
PRINTS; PR00416; CCAATSUBUNTA.
PRINTS; PR00416; TP12FAMILY.
ProDom; PD000742; DNA_topoisolV; 1.
SNART; SM0043; TOP2c; 1.
SNART; SM0043; TOP2c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:98790; Top2a.
InterPro; IRR003594; ATPbind ATFase
InterPro; IRR003594; ATPbind ATFase
InterPro; IRR001241; INA topoisoIIV.
InterPro; IRR002205; DNA_topoisoIV.
                                MEDLINE=93065194; PubMed=1331984;
                                                                                                                                                                                                                                                                                                              MEDLINE=94084643; PubMed=8261398;
                                                                                                                                                                                                                                          SEQUENCE OF 1254-1528 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.6%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U01915; AAC52135.1; -. PIR; JS0703; JS0703. HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D12513; BAA02076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
```

ö

Gaps

ö

3,

Conservative

임

Search completed: January 29, 2004, 12:39:07 Job time : 8.28947 secs

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein -

on:

```
Ogyg15 schizosacch Ol715 procambarus Ol714 procambarus Ol714 procambarus Ol714 procambarus Ol715 procambarus Ol715 procambarus Ogyg21 anabaena sp. Ogyg21 arrowia 11 Ogyg21 p. Oyyg21 arrowia 11 Ogyg21 p. Oyyg21 arabidopsis Oghre arabidopsi
Q8ehb9 shewanella
Q9kbj7 bacillus ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
MATRIX EXTRACELLULAR PHOSPHOGLYCOPROTEIN.
0977CA6E871CA9E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nomo sapiens (ruman).
Bukaryota, Metazoma, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=21309068; PubMed=11414762;

Argiro L., Desbarats M., Glorieux F.H., Ecarot B.;

Argiro L., Desbarats M., Glorieux F.H., Ecarot B.;

"Mepe, the gene encoding a tumor-secreted protein in oncogenic hypophosphatemic osteomalacia, is expressed in bone.";

Genomics 74:342-351(2001).

EMBL; AJ276396; CAB97250.1; -..

EMBL; AF325916; AAK70343.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20399567; PubMed-10945470; Rowe P.S.N., De Zoysa P.A., Dong R., Wang H.R., White K.E., Econs M.J., Oudet C.L.; MEDER & new gene expressed in bone marrow and tumors causing osteomalacia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Matrix extracellular phosphoglycoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82; DB 4; I
Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                      Q9P9M4
Q8IUP7
                                                                                                                                                                                                                Q9VF03
O10378
                                                                                                                                                                                                                                                                                                                                                                 Q9LHE9
Q9SHZ7
Q8Z5E7
Q97YV0
Q91798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9A7E1
Q9XE29
                                                                                                                                                     Q98HC0
Q8R3S4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VA07
Q8GT32
                                                                                                                                                                                                                                                                                                              Овремо
                                                                                                                                                                                                                                                                                                                                 O9SNF0
                                                                                                                                                                                                                                                                                                                                                 QBRWT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 MJ
58419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
     PRELIMINARY;
   1007
4444
629
1002
1020
430
430
430
702
1002
1002
663
                                                                                                                                                                                                                                                                                            osteomalacia.";
Genomics 67:54-68(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
18 5
525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone;
                                                                                                                                                                                                                                                                                                              444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09NQ76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09N076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
     97<u>0</u>N60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q24ii mus musculu
Q98802 rattus norv
Q8K416 mus musculu
Q8K3v0 rattus norv
Q8nc19 homo sapien
Q8vik4 mus musculu
Q912w8 mus musculu
Q9gq03 ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8yi83 brucella me
Q8fzn1 brucella su
29c091 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95kg5 macaca fasc
Q9n076 macaca fasc
Q9gml3 macaca fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9nq76 homo sapien
O95kg5 macaca fasc
O9n076 macaca fasc
                                                                                                                                   January 29, 2004, 12:35:53; Search time 22.1053 Seconds (without alignments) 175.107 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                         830525
                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.99NQ76
0.95KG5
0.95KG5
0.95KG5
0.95KG5
0.95KG1
0.95KG1
0.85KG4
0.85KG1
0.80KG1
0.80K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8Y183
Q8FZN1
Q9C091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPTREMBL_23:*
1: sp archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_tungi:*
5: phuman:*
5: sp_invertebrate:*
5: sp_mammal:*
5: sp_mammal:*
5: sp_mhc:*
                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unclassified: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                    1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                        US-09-812-485A-47
82
                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rodent: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_plant: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        886.6
886.6
733.2
84.9
54.9
54.9
54.9
```

Result No.

4 4 4

RESULT 2

ò g 995KGS 999 BT 990 BT

```
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATRIX EXTRACELLULAR PHOSPHOGLYCOPROTEIN.; 7CD603CAA8CB41B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                              MEPE protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mamalia; Butheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J;
MEDLINE=21309068; PubMed=11414762;
Argiro L., Desbarats M., Glorieux F.H., Ecarot B.;
"Mepe, the gene encoding a tumor-secreted protein in oncogenic hypophosphatemic osteomalacia, is expressed in bone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                          96.3%; Score 79; DB 6; Length 555
93.3%; Pred. No. 4.5e-05; O. Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 11; Length 43
Pred. No. 0.00081;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                             libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB050259; BAB17010.1;
SEQUENCE 555 AA; 61950 MW; BD4D47E88038A9E2 CRC64;
                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Matrix extracellular phosphoglycoprotein precursor.
                                       555 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 74:342-351(2001).
EMBL; AF314964; AAK70342.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 M.
45984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 ERGDNDMSPFSGDGQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ERGDNDISPESGDGO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||: ||||||
175 RGDNDVPPFSGDGQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.3'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.6
Best Local Similarity 85.7
Matches 12, Conservative
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:2137384; Mepe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
19 4
433 AA;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
SIGNAL
                                     Q9GM13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        092411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ES02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
Q9ES02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
RESULT 4
                   29GM13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2924I1
                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Temporal cortex;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Obsada M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 55.6 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Mammalia; Butheria; Primates; Craniata; Vertebrata; Buteleostomi; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Matrix extracellular phosphoglycoprotein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79; DB 6; Length 555;
Pred. No. 4.5e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%; Score 79; DB 6; Length 500; 93.3%; Pred. No. 4e-05;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          libraries.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB060891; BAB46894.1; -.
Hypothetical protein.
SEOUENCE 500 AA; 55577 MW; 918D265AD8EDC7BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                libraries.", Submitted (ULL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AB046056; BAB01638.1; SEQUENCE 555 AA, 61979 MW; CCFE1A98ADA19EE4 CRC64;
                                                                                                                                                                       500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
Mismatches
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.3%;
                                                                         246 ERGDNDISPESCOGO 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRGDNDMSPFSGDGQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERGDNDMSPFSGDGQ 291
                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ERGDNDISPESGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                     1 ERGDNDISPFSGDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
 15; Conservative
                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222
                                                                                                                                                                         Q95KG5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910N6Q
 Matches
```

g

ò

ö

Gaps

ö

ô

Gaps

ö

```
Wang X., Hu B., Wang Y.; "Reattus norvegicus con CDNA sequence expressed in B4 cell line (possible "Rattus norvegicus convegitus con Subrype of osteoregulin) "; subrype of otto-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Placenta;

TISSUE-Placenta;

TISSUE-Placenta;

TORAT, Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suuzki Y., Nagai T., Ota T., Nishikawa T., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Sasaki N., Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 86.6%; Score 71; DB 11; Length 443; Local Similarity 85.7%; Pred. No. 0.00083; es 12; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 73.2%; Score 60; DB 4; Length 275; al Similarity 91.7%; Pred. No. 0.038; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF530559; AAM94404.1; -. SEQUENCE 443 AA; 47672 MW; 720EEC4C0718FB14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 275 AA; 31358 MW; AF0B426A671B665C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
10-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ90595.
                                                                   QBK3V0;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Osteoregulin-like procein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 AA
                                         443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 20, 1 (TrEMBLrel. 20, 1 (TrEMBLrel. 23, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 RGDNDVPPFSGDGQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 ERGDNDISPFRG 257
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ERGDNDISPFSG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (01-MAR-2003 (01-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=F344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8NC19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VIK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
Q8VIK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
08K3V0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBNC19
                                                                           AC OCC OCC OCT REPRESENTED THE SECOND THE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-F344;

Hu B., Wang X., Wang Y.;

Hu B., Wang X., Wang Y.;

Rattus norvegicus CDNA sequence highly expressed in A1-5 cell line (identical to osteoregulin).";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF260922; AAG33366.1; -.

EMBL; AF30558; AAM94403.1; -.

SEQUENCE 435 AA, 46515 MW; DS87F82968A26BCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gowen L.C., Petersen D.N., Vail A.L., Stock J., Tkalcevic G.T., Simmons H.A., Chidsey-Frink K.L., Ke H., McNeish J., Brown T.A.; "Targeted disruption of the osteoregulin gene results in increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley;
MEDLINE=20549633; PubMed=10967096;
Petersen D.N., Tkalcevic G.T., Mansolf A.L., Rivera-Gonzalez R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown T.A.;
"Identification of Osteoblast/Osteocyte Factor 45 (0F45), a Bone specific cDNA Encoding an RGD-containing Protein That Is Highly Expressed in Osteoblasts and Osteocytes.";
J. Biol. Chem. 275:36172-36180(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
86.6%; Score 71; DB 11; Length 435;
1 Similarity 85.7%; Pred. No. 0.00081;
12; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.6%; Score 71; DB 11; Length 441;
85.7%; Pred. No. 0.00083;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone density.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF298661; AAM87687.1; -.
MGD; MGI:2137384; Mepe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46872 MW; AA1947BFE9F2E300 CRC64;
                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 RGDNDVPPFSGDGQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGDNDVPPFSGDGQ 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                 Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osteoregulin.
                                                                                                                                                           Osteoregulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

**08K4L6** 

RESULT 7
0844L6
0844L6
0010
01-001-0
01-001-0
01-001-0
02 Mus Oste
03 Mus Oste
05 Wus Oste
06 Wus Oste
07 Wus Oste
08 Wus Oste
09 Wus Oste

RESULT

ò

Matches

윱

ö

Gaps

ö

ô

Gaps

ö

```
Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holf W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Button G.G., Wortman J.K., Yandall M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Batter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
A Man K.H., Boyle C., Batter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Boude, J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis B.P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis B.P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Dodson K., Devisilian A.E., Gargy N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Hermandez J.R., Housen C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lasko P., Li J., Li Z., Liang Y., Lin X.,
A Liako P., Mattei B., McIntosh T.C., McLeod M.P., McConstruction D.,
                                                                                                                                                                                                                                                                                                           Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen B.Y., Cassell G.H.;
                                                                                                                                                              Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma. NVCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 16; Length 913;
Pred. No. 56;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                               The complete seguence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              913 AA; 106010 MW; FE9AD007C44AE0E3 CRC64;
                                                                                                                                                       Ureaplasma parvum (Ureaplasma urealyticum biotype 1)
                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
913 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                        STRAIN=Serovar 3; MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                    urealyticum.";
Nature 407:757-762(2000).
EMBL; AE002146; AAF30899.1;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   891 NDISPESKODQ 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 NDISPFSGDGQ 15
                                                                                                            MBA N-terminal paralog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG14085 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VVY0
                                                                                                                                    UU487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.XAA60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11581173;
Park C.G., Takahara K., Umemoto E., Yashima Y., Matsubara K.,
Matsuda Y., Clausen B.E., Inaba K., Steinman R.M.;
"Five mouse homologues of the human dendritic cell C-type lectin, DC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.9%; Score 45; DB 11; Length 207; 66.7%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.9%; Score 45; DB 11; Length 237; 66.7%; Pred. No. 12; 3; Indels ive 1; Mismatches 3; Indels
                                                                                                                                                                              Park C.G., Steinman R.M.;
"Alternatively Spliced Forms of Mouse DC-SIGN Homologs.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF440280; AAL33584.1; --
MGD; MGI:2157947; CD2094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Int. Immunol. 13:1283-1290(2001).

EMBL; AF37341; AAL13237.1; -

MGD; MGI:2157947; CD2040.

InterPro; IRR001304; Lectin_C.

Ffam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00041; CTYPE_LECTIN 1; 1.

PROSITE; PS0041; CTYPE_LECTIN 2; 1.

SROUSTE; PS50041; CTYPE_LECTIN 2; 1.

SROUENCE 237 AA; Z6925 MW; 52E3003C65AF9EF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 207 AA; _23500 MW; 16FB45EB47ECAD3FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                        InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMRITS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Query Match
Best Local Similarity 66.7.,
Best Local Similarity 67.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 GDEDCAEFSGDG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GĎEĎCAEFSGĎG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 66.7
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDNDISPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GDNDISPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD209D OR SIGNR3.
                                                                                       NCBI_TaxID=10090;
  CD209D OR SIGNR3
                                                                                                                                                           STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
```

0912W8 Q91ZW8

RESULT 11 Q91ZW8

à

SIGNR3

ო

ð

RESULT 12 Q9PQ03

SIGN.";

ö

.. 0

SEQUENCE Query Match

23, Created)

```
completed: January 29, 2004, 12:40:17
ne : 24.1053 secs
                                                                                                                                                                              Brucella suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rigr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Job time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search
           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N [1]
SEQUENCE FROM N.A.
REDLINE=20020109; PubMed=11756688;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA DelVecchio V.G., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT The glam melitensis ";
RY Natl. Acad. Sci. U.S.A. 99:443-448(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier B., Siden-Käamos I., Simpson M., Skupski M.P., Smith T.,
Spier B., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
We J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,
Cibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000)
REMBL, AEOROSIST?, AAR49175.1;
REMBL, AEOROSIST?, AAR49175.1;
REMBL, REDOMO35619, GC14085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.3%; Score 44.5; DB 5; Length 793; 71.4%; Pred. No. 58; ive 0; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 16; Length 277;
Pred. No. 22;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brucella melitensis.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Нуdrolase; Glycosidase; Complete proteome.
SEQUENCE 277 AA; 31766 МW; ВӨІСР4ВА63E92BB0 СRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Lysozyme M1 precursor (EC 3.2.1.17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:443-
EMBL; AE009498; AAL51743.1; -
InterPro; IPR002053; Glyco_hydro_25.
Pfam; PF01183; Glyco hydro_25.
Probom; PD004620; Glyco hydro_25; I.
SWART; SW00641; Glyco_25; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDNDPSPFOGIOGO 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GDNDISPFSG-DGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| ||: |:||
252 RGDADINTFAGD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.4
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RGDNDISPFSGD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brucellaceae; Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8YI83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
008Y183
10 01-MA
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
           ò
```

277 AA.

PRT;

PRELIMINARY;

Q8FZN1 RESULT 15 Q8FZN1 ID Q8FZN

셤

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Heidelberg J.F.,
                                                                                                                                                                                                                                                                                                                STRAIN=1330 / Blovar 1;
STRAIN=1330 / Blovar 1;
MEDLINE=222711122;
MEDLINE=2227741; PubMed=12271122;
MEDLINE=2227741; PubMed=12271122;
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Akne S.I.
Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
"The Brucella suis genome reveals fundamental similarities between annimal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       watch 53.7%; Score 44; DB 16; Length 277; Local Similarity 66.7%; Pred. No. 22; es 8; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase, Complete proteome.
SEQUENCE 277 AA; 31750 MW; B81CF4BA7E28F7B0 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                           Glycosyl hydrolase, family 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE014440; AAN30360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - ||| ||: |:||
252 RGDADINTFAGD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RGDNDISPFSGD 13
                                                                                                                                                                                                                                                    NCBI_TaxID=29461;
```

THIS PAGE BLANK (USPTO)

```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                     January 29, 2004, 12:34:18; Search time 42.9737 Seconds (without alignments) 84.952 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | SIDSI/gegdata/geneseq/geneseqp_emb1/AA1992.DAT:+
| SIDSI/gegdata/geneseqgeneseqp_emb1/AA1993.DAT:+
| SIDSI/gegdata/geneseqgeneseqp_emb1/AA1993.DAT:+
| SIDSI/gegdata/geneseqgeneseqp_emb1/AA1994.DAT:+
| SIDSI/gegdata/geneseqgeneseqp_emb1/AA1995.DAT:+
| SIDSI/gegdata/geneseqgeneseqp_emb1/AA1999.DAT:+
| SIDSI/gegdata/geneseqgeneseqp_emb1/AA1999.DAT:+
| SIDSI/gegdata/geneseqgeneseqgeneseqp_emb1/AA1999.DAT:+
| SIDSI/gegdata/geneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgeneseqgenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | SIDSI/gogdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gogdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/gogdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDSI/gogdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDSI/gogdata/geneseq/geneseqp-embl/AA1986.DAT:*
| SIDSI/gogdata/geneseq/geneseqp-embl/AA1986.DAT:*
| SIDSI/gogdata/geneseq/geneseqp-embl/AA1987.DAT:*
| SIDSI/gogdata/geneseqf/geneseqp-embl/AA1988.DAT:*
| SIDSI/gogdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDSI/gogdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDSI/gogdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDSI/gogdata/geneseqf/geneseqp-embl/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Geneseq 19Jun03:*
: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1107863
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-812-485A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                 Run on:
```

					SOMMAKIES	
		مه				
Result,		Query				
No.	Score	Match	Match Length DB ID	DB	ΠD	Description
-	126	100.0	23	23	AAU93726	Dental product bon
~	126	100.0	23	23	AA020379	C-terminal amidate
М	126	100.0	97	23	AAU93681	Dental product bon
4	126	100.0		23	AA020331	Protein of matrix
ß	126	100.0	430	21	AAY53812	Amino acid sequenc
9	126	100.0		22	AAB62669	Truncated phosphat
7	,126	100.0		22	AAB82922	Human osteoregulin
89	126	100.0		22	AAB82920	Human osteoregulin
σ	126	100.0		22	AAB62689	Phosphatonin polyp

Human phosphatonin Human oncogenic os Human osteoregulin Human osteoregulin Protein of matrix Human OOM1 calcium Dental product bon C-terminal amidate Dental product bon Peptide of matrix Dental product bon C-terminal amidate C-terminal amidate Rat osteoregulin. Mouse osteoregulin.	Human polypeptide,  C-terminal amidate Dental product bon Protein of matrix Dental product bon Peptide of matrix Dental product bon Protein of matrix Dental product bon Protein of matrix Human bone matrow Human phospholipas Human phospholipas Human lipase NHL (Human lipase NHL (Human lipase NHL (Human lipid-associ	ENTS peptide #46.	sh; dental floss; bone growth; al disease; dental disease; tooth; adontoblast; osteopathic. skeletal diseases e.g. dental and a compound comprising specific
ABB08526 AAE13227 AAB82923 AAB82923 AAU93703 AAC20353 AAC20353 AAC20378 AAU93724 AAU93724 AAU93724 AAU93724 AAU93724 AAU93724	AAM935207 AAU93723 AAU93723 AAU93706 AA020356 AA020356 AAU93705 AAU93705 AAU93705 AAU93705 AAU93705 AAU93705 AAU93705 AAU93705 AAU93705 AAU93707 AAC20355 AAC20355 AAC20357	ALIGNMENT 23 AA. enhancing pep	; mouthwash; of skeletal dioblast; odonting.  11.  12.  13.  14.  15.  16.  17.  19.  18.  19.  19.  19.  10.  10.  10.  10.  10
555555555555555555555555555555555555555	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ъ ~ e	
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	275 155 160 175 175 175 175 175 175 175 175 175 175	; pept st ent ne gro	thp tiff h; -US -222 ', '
	00000000000000000000000000000000000000	ar fi	oduct, too binding mo bone growt .: .75-A1. 001, 2001WO 000, 2000US NOMIZU M i-329525/36 coduct usef
	80 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	93726 st 93726; JUL-2002	egrin bi eclar bo eclar bo thetic. 00213775 FEB-2002 AUG-2001 GB-) BIG eda T, ; 2002-3 tal prod
	00000000000000000000000000000000000000	T. 72 AA AA O2	XX XW intr XW alv, XX XX XX XX XX XX YX YX YX YX YX YX YX

ö

Gaps

; 0

Indels

Query Match Best Local S

Matches

g

ð

Sequence

F X X X D D D D D D D D D D X X

23;

Length

```
motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts /osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a C-terminal amidated synthesised peptide D-00006 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of osteoblast or odontoblast cells on the surface of the new skeletal growth. AAU33681-AAU33726 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                                                                                                                                                                                                                                 Score 126; DB 23;
Pred. No. 2e-12;
: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 126; DB 23;
100.0%; Pred. No. 1.1e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dental product bone growth enhancing peptide #1.
                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                           1 TDLOERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 11; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU93681 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000; 2000US-225879P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001; 2001WO-US25101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIGB-) BIG BEAR BIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-329525/36.
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                              23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200213775-A1.
                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoneda T,
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU93681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                               The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of esteoblast or adontoblast cells on the surface of the new skeletal growth. AAU33681-AAU33726 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; weakness; D00006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide compound useful for reducing bone loss, is capable enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
0
            amino acid in a sequence containing the integrin binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 126; DB 23; Length 23; 100.0%; Pred. No. 2e-12; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-terminal amidated synthesised peptide D-00006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blacher RW, Yoneda T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 15; 50pp; English.
                                                          Claim 7; Page 21; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO20379 standard; peptide; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2001; 2001WO-US25542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2000; 2000US-0641034.
19-MAR-2001; 2001US-0812485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIGB-) BIG BEAR BIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-291971/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200214360-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kumagai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2002
```

Synthetic

AA020379;

ö

Gaps

. 0

Indels

Length 97;

ઠે g

```
Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a peptide compound capable of enhancing bone scrowth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D-or L-conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing regard phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a protein of a matrix extracellular phosphoglycoprotein containing an RGD motif of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                          Bone growth, RGD motif, integrin binding motif, calcium binding motif, glycosaminoglycan binding motif, bone loss, renal phosphate excretion, alveolar, teeth, odontoblast, osteoclast, dental tissue, skeletal loss,
                                                                                                                                                                                                                                                                                                                                                         Protein of matrix extracellular phosphoglycoprotein containing RGD #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             weakness; matrix extracellular phosphoglycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 126; DB 23;
100.0%; Pred. No. 1.1e-11;
ive 0; Mismatches 0;
                               43 TDLQERGDNDISPFSGDGQPFKD 65
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 11; 50pp; English.
                                                                                                                                                                                            AAO20331 standard; protein; 97 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kumagai Y, Blacher RW, Yoneda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2001; 2001WO-US25542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000; 2000US-0641034.
19-MAR-2001; 2001US-0812485.
                                                                                                                                                                                                                                                                                                   31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIGB-) BIG BEAR BIO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-291971/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200214360-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2002.
                                                                                                                                                                                                                                               AA020331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                  AA02033
```

TDLQERGDNDISPFSGDGQPFKD 65

43

유 ò

AAY53812 standard; Protein; 430 AA

RESULT 5
AAY53812
ID AAY5.
XX
AC AAY5.

AAY53812

TDLQERGDNDISPFSGDGQPFKD 23

```
MEPE; Na+-dependent phosphate cotransport; vitamin D metabolism; bone mineralisation; phosphate metabolism related disease; hyperphosphatemia; renal osteodystroppy; renal dislysis; secondary hyperparathyrodism; osteitis fibrosa cystica; hypercalcuria; X-linked hypephosphatemic ricket; hereditary hypophosphatemic ricket; hypomineralised bone lesion; stunted growth; cystic fibrosis; oncogenic hypophophatemics osteomalacia; renal phosphate leskage; renal osteodystrophy; osteoporosis; vitamin D resistant rickets; end organ resistance; renal Fanconi syndrome; autosomal rickets; paget's disease; kidney failure; renal tubular acidosis; sprue.
                                                                                                                          Human; phosphatonin; Metastatic-tumour Excreted Phosphaturic-Element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..10
note= "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..202
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8..11
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228. 231
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.47
/note= "Tyrosine kinase phosphorylation site"
/note= "protein kinase C phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "protein kinase C phosphorylation
                                                                         Amino acid sequence of a human phosphatonin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "cell attachment tripeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228..230
/note= "p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161..165
/note= "g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291..296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 . . 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . . 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312..314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370..373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238..241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note≈
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     notes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
THE SELECTION OF S
```

4

147 TDLQERGDNDISPFSGDGQPFKD 169

1 TDLQERGDNDISPFSGDGQPFKD

8 a AAB62669 standard; Protein; 430 AA

AAB62669

23

```
The present sequence represents a phosphatonin polypeptide (also called Metastatic-tumour Excreted Phosphaturic-Element (MEPE). The level of phosphaton in a subject modulates Na+-dependent phosphate corransport, vitamin D metabolism and/or bone mineralisation. The phosphatonin to polypeptides, polymucleotides, vectors and antibodies are used to treat phosphate metabolism related disease. They are used for treatment of hyperphosphatemia, or renal osteodystrophy, hyperphosphatemia in renal dalysis/pre-dialysis, secondary hyperparathyrodism or ostetis fibrosa cystica, or X-linked hypophosphatemic rickets, hereditary hypophosphatemic rickets with hyperalcuria (HRRH), hypominaralised hypophosphatemic rickets with hyperacilcuria (HRRH), hypominaralised costeomalacia, renal phosphate leakage, renal osteodystrophy, osteomalacia, vitamin D resistent rickets, end organ resistance, renal ranches, autosomal rickets, end organ resistance, renal ranches, autosomal rickets, end organ resistance, renal tubular acidosis, cystic fibrosis or sprue. The polypeptide may also be used to manifacture combined preparations for simultaneous, desparate or sequential use for the treatment of phosphate metabolism disorders. A transformed osteoblast or bone cell line capable of the characterial or special for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides involved in the regulation of phosphate metabolism useful for diagnosing and treating disorders related to phosphate
                                                                                               "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                           425..428
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                             "protein kinase C phosphorylation site"
                                                                                                                                                                                               /note= "cAMP and cGMP dependent protien kinase
                                                                                                                                                                                                                                             "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                            "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                              "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                           /note= "Casein kinase II phosphorylation site"
                                "Asu-glycosylation site"
                                                                'note= "Asu-glycosylation site"
                                                                                                                                                                                                                phosphorylation site'
                                                                                                                               "myristoylation site"
/note= "amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Fig 8; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNLO ) UNIV COLLEGE LONDON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-EP03403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98GB-0010681
98GB-0019387
                                                                                                                                                                                                                                                                                           ..426
                                             .387
                                                                                                                                              ..405
                                                                                                                                                                              .408
                382..386
                                                                               384..386
                                                                                                            389..394
                                                                                                                                                                                                                                                            409..411
                                                                                                                                                                                                                                                                                                                                                             .430
                                                                                                                                                               /note=
405..40
                                                                                                'note=
                                 note=
                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-053262/04.
N-PSDB; AAZ36447.
                                                                                                                                                  403
               Modified-site
                                             Modified-site
                                                                            Modified-site
                                                                                                            Modified-site
                                                                                                                                            Modified-site
                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                             WO9960017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rowe P;
```

/note= "the amino acid residues in this region are indicated incorrectly in the sequence provied

Location/Qualifiers

Misc-difference 161..192

Homo sapiens.

in the sequence listing'

31-OCT-2000; 2000WO-EP10747

WO200132878-A2

10-MAY-2001.

99US-0434185 99GB-0026424

04-NOV-1999; 08-NOV-1999;

(UNLO ) UNIV COLLEGE LONDON

WPI; 2001-343487/36. N-PSDB; AAF83759.

Rowe P;

Metastatic-tumour excreted phosphaturic element; MEPE; phosphatonin; phosphate; vitamin-D; skeletal formation; mineralization; truncated; osteopathic; antigout; cytostatic; human.

Truncated phosphatonin polypeptide (truncated MEPE).

(first entry)

23-JUL-2001

AAB62669;

```
The invention relates to a novel human protein, metastatic-tumour excreted phosphaturic element (MEPE) or phosphatonin (modulator of phosphate and vitamin-D metabolism). The phosphatonin polypeptides, polymucleotides and specific antibodies are useful for treating a disorder of phosphate or vitamin D metabolism, skeletal formation and mineralization. Phosphatonins are used to treat hyperphosphatemia, renal osteodystrophy, secondary hyperparathyroidism, osteitis fibrosa cystica or gout. It is used to prepare a medicament for treating X-linked hyperposphosphatemic rickets, hereditary hyperposphatemic rickets with hypercalcuria (HHRH), hypomineralized bone lesions, stunted growth in juveniles, oncogenic hypophosphatemic osteomalacia, renal phosphatemic organ resistance, renal fanconi syndrome, autosomal rickets, paget's cand organ resistance, renal tubular acidosis, cystic fibrosis or spruce. Phosphatonin polymorlocides are useful as molecular weight markers on Southern gels, as diagnostic probes for detecting the presence of a specific mRNA. Phosphatonin polypeptides are also useful for cidentifying agonists and antagonists compounds which bind to phosphatonin and drug candidates for therapy of phosphate metabolism choosing a truncated form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New phosphatonin polypeptide a regulator of phosphate metabolism, for diagnosing and treating disorders of phosphate, vitamin-D metabolism, skeletal formation e.g. osteoporosis, Paget's disease, gout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 8; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatonin (MEPE)
```

430 AA;

Sequence

ö

Gaps

; 0

ch 100.0%; Score 126; DB 21; Length 430; 1 Similarity 100.0%; Pred. No. 5.8e-11; 23; Conservative 0; Mismatches 0; Indels 0

Query Match Best Local Similarity

Matches

430 AA;

Sequence

phosphatonin.

23

S

us-09-812-485a-49.rag

```
1 TDLQERGDNDISPFSGDGQPFKD
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                 EP1130098-A2
                                                                                                                                                                                                                                                                                                                                                         05-SEP-2001
                                                                                                          AAB82920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                           therapy.
                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                              Protein
                                                           RESULT 8
                                                                        4AB82920
                                                                                                          8
                      ద
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of human osteoregulin mature polypeptide, i.e. lacking an N-terminal signal sequence.
Colseoregulin is a novel protein which plays a roole in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. 2 Splice variants of human osteoregulin exer identified (see also AAB82921). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, animal cells and mammals with a targeted disruption of an enimal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with in the manufacture of a medulators of activity may be useful in the manufacture of a medulators of activity may be useful in the manufacture of a medulators of activity may be useful mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin -
                                   Gaps
                                                                                                                                                                                                                                            Osteoregulin, human, bone, homeostasis, adipose, calcification, atherosclerosis, osteoporosis, osteopathic, antiarteriosclerotic;
                                  ô
           Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 509;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 126; DB 22;
100.0%; Pred. No. 7.1e-11;
iive 0; Mismatches 0;
          Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e-11;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Нашев ГМ
                                                                                                                                                                                                                    Human osteoregulin (mature polypeptide).
                                                                           147 TDLQERGDNDISPFSGDGQPFKD 169
                                                          1 TOLOERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 54-55; 90pp; English.
                                                                                                                                             AAB82922 standard; Protein; 509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gowen LC,
                                                                                                                                                                                                                                                                                                                                                                                            29-FEB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2001; 2001EP-0301768
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-604111/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH26810.
                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                             21-DEC-2001
                                                                                                                                                                                                                                                                                                                    EP1130098-A2
                                                                                                                                                                                                                                                                                                                                             05-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown TA,
                                                                                                                                                                      AAB82922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                       therapy.
                                                                                g
                                                                                                                                                         ð
```

```
which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclarotic plaques. The sequence is considered from the mucleotide sequence (see AA126808) of isolated predicted from the nucleotide sequence (see AA126808) of isolated costeoblast cDNA. A spile avainat of human osteoregulin was also identified (see AA882921). The invention provides novel costeoregulin proteins, nucleic acids which encode them, vectors, antibodies, host calls which express heterologous osteoregulins, and canimal cells and mammals with a targeted disruption of an costeoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, canamal in need of regulation of bone mass and/or density, and/or atherosciencic plaque calcification (claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is that of human osteoregulin, a novel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoregulin; human; bone; homeostasis; adipose; calcification; atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 126; DB 22; Best Local Similarity 100.0%; Pred. No. 7.3e-11; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gowen LC, Hames LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38..525
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Signal_peptide
226 TDLQERGDNDISPFSGDGQPFKD 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 45-47; 90pp; English.
                                                                                                                                                                                                                              AAB82920 standard; Protein; 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-FEB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-2001; 2001EP-0301768
                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown TA, De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-604111/69.
N-PSDB; AAH26808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human osteoregulin.
```

ô

ö

Gaps

ö

Indels

242 TDLQERGDNDISPFSGDGQPFKD 264

Ā

셤

ò

```
Human phosphatonin; cytostatic; antidiabetic; antiinflammatory; hyperphosphaemia; arteriosclerosis; heart failure; diabetic renal disease; kidney failure; cystic fibrosis.
                                                                                                            ABB08526 standard; protein; 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-2000; 2000JP-0191088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-2001; 2001WO-JP05263
                                                                                                                                                                                                                                               Human phosphatonin.
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200198495-A1.
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurokawa T,
                                                                                                                                                                                                 23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-DEC-2001
                                                                                                                                                        ABB08526;
                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sprue. Phosphatonin polynucleotides are useful as molecular weight markers on Southern gels, as diagnostic probes for detecting the presence of a specific mRNA. Phosphatonin polypeptides are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel human protein, metastatic-tumour excreted phosphaturic element (MEPE) or phosphatonin (modulator of phosphate and vitemin-D metabolism). The phosphatonin polypeptides, polynucleotides and specific antibodies are useful for treating a disorder of phosphatonins are used to treat hyperphosphatemia, mineralization. Phosphatonins are used to treat hyperphosphatemia, renal osteodystrophy, secondary hyperparathyroidism, osteitis fibrosa cystica or gout. It is used to prepare a medicament for treating X-linked hypercalcuria (HHRH), hypomineralized bone lesions, stunted growth in hypercalcuria (HHRH), hypomineralized bone lesions, stunted growth in juveniles, oncognic hypophosphatemic osteomalacia, renal phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leakage, renal osteodystrophy, osteoporosis, vitamin-D resistant rickets, end organ resistance, renal Fanconi syndrome, autosomal rickets, Paget's disease, kidney failure, renal tubular acidosis, cystic fibrosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identifying agonists and antagonists, compounds which bind to phosphatonin and drug candidates for therapy of phosphate metabolism disorders. The present sequence represents the amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New phosphatonin polypeptide a regulator of phosphate metabolism, for diagnosing and treating disorders of phosphate, vitamin-D metabolism, skeletal formation e.g. osteoporosis, Paget's disease, gout
                                                                                                                                                                                                                                                                                                                                  Metastatic-tumour excreted phosphaturic element; MEPE; phosphatonin; phosphate; vitamin-D; skeletal formation; mineralization; truncated; osteopathic; antigout; cytostatic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 22; Length 525; 100.0%; Pred. No. 7.3e-11; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 133-134; 135pp; English
                                242 TDLQERGDNDISPFSGDGQPFKD 264
  23
                                                                                                                                                          AAB62689 standard; Protein; 525 AA.
  1 TDLQERGDNDISPFSGDGQPFKD
                                                                                                                                                                                                                                                                                         Phosphatonin polypeptide (MEPE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders. The present sequenc
the entire phosphatonin (MEPE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0434185.
99GB-0026424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNICO ) UNIV COLLEGE LONDON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000; 2000WO-EP10747.
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-343487/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAF83764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200132878-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-1999;
                                                                                                                                                                                                                                               23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rowe P;
                                                                                                                                        AAB6268
```

T, Morimoto S;

Yamada

```
ö
                                                                                                                                                                                                                                                                                                          the activity of lowering blood phosphate and increasing urinary phosphate. The proteins are cytostatic, antidabetic and antiinflammatory in their action. Phosphatonin down-regulates sodium-dependent phosphate transport in the kidney, it down-regulates 25-hydroxy-vitemin D3-1alpha-hydroxylase in the kidney and up-regulates 25-hydroxy-vitemin D3-24-hydroxylase in the kidney. Phosphatonin is useful in the diagnosis, treatment and prevention of phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolism related diseases such as hyperphosphaemia, arteriosclerosis, heart failure, diabetic renal disease, kidney failure, acute coronary disease and cystic fibrosis. This sequence represents human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                             Phosphatonin of human origin and DNA encoding it for diagnosis and treatment of diseases associated with disorders of phosphate metabolism, e.g., hyperphosphaemia, arteriosclerosis, heart failure, diabetic renal disease and kidney failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                This invention relates to human phosphatonin which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 126; DB 23;
100.0%; Pred. No. 7.3e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 TDLQERGDNDISPFSGDGQPFKD 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE13227 standard; Protein; 525 AA.
                                                                                                                                                                                                                             Claim 1; Fig 1-4; 130pp; Japanese.
                       N-PSDB; ABA99159, ABA99160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
WPI; 2002-139791/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphatonin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE13227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE13227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 X Y X 1
```

Local Similarity 100. nes 23; Conservative

0

Gaps

. 0

```
ద
 888888888888
                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to oncogenic osteomalacia-related protein 1
designated OOM1 (oncogenic osteomalacia-related factor) and its DNA
molecule. OOM1 protein is useful for treating a phosphate homeostasis-
related disease such as X-linked hypophosphateamia rickets, oncogenic
osteomalacia, rhabdomyolysis, cardiomyopathy, tumoural calcinosis and
renal failure. OOM1 proteins and DNA's are useful for modulating the
C phenotype of a neoplastic cell associated with oncogenic osteomalacia,
modulating bone mineralisation; and treating a disease characterised by
abnormal bone mineralisation; and treating an oncogenic osteomalacia-
c associated symptom auch as hypophosphateamia, phosphaturia, low serum
concentrations of 1.25-dihydroxy vitemin D or osteomalacia. OOM1 is
useful for modulating renal phosphate transport, which involves altering
the activity of OOM1 within a cell and then administering serine protease
11 to the cell OOM1 within a cell and dentifying single nucleotide
animal models, and for searching and identifying single nucleotide
polymorphisms which are mutants, variants of the gene in human
                                                                                                                                                                                 /label= Signal_peptide
17..525
/note= "Mature oncogenic osteomalacia-related protein-l
                                           Human, oncogenic osteomalacia-related protein 1; OOM1; gene therapy; phosphate homeostasis-related disease; ritketej osteomalacia; cardiant; rhabdomyolysis; cardiomyopathy; tumoural caldinosis; renal failure; bone mineralisation; phosphaturia; cellular process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding a polypeptide useful for identifying polynucleotide expression or polypeptide activity modulators used treating oncogenic osteomalacia, comprises the oncogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Bacterial extracellular solute-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jan De Beur
                                                                                                                                                                                                                                                                                                                                                                                                                   "Potential PKA phosphorylation site"
               Human oncogenic osteomalacia-related protein-1 (OOM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Manavalan P, Levine MDM,
                                                                                                                                                                                                                                                             /note= "Calcium binding motif"
235..258
                                                                                                                                                                                                                                                                                                                                      264..275
/note= "Calcium binding motif"
                                                                                                                                                                                                                                                                                                                                                                /mcre= "Calcium binding motif"
                                                                                                                                                                                                                                                                                           "Calcium binding motif"
                                                                                                                                                                                                                                                                                                                        "Cell attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Glycosylation site"
                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 2; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-2000; 2000US-191786P.
19-OCT-2000; 2000US-241598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2001; 2001WO-US09289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENZYME CORP.
UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteomalacia-related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500..503
                                                                                                                                                                                                                                                                                                          . . 249
                                                                                                                                                                                                                                                                                                                                                                                                                                   477..481
                                                                                                                                                                                                                                                130..142
                                                                                                                                                                                                                                (00M-1) "
                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schiavi S, Madden S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-010720/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200172826-A2
                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                         Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2001
                                                                                                                                                       Key
Peptide
                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENZ
(UYJO
                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                          Region
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of human osteoregulin mature polypeptide, i.e. lacking an N-terminal signal sequence.

Colsteoregulin is a novel protein which plays a role in regulating costeoregulin is a novel protein which plays a role in regulating concerning a diposity, and the calcification of atherosclerotic plaques. 2 Splice variants of human osteoregulin were identified (see also AAB2292). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, antibodies, host cells which express heterologous osteoregulins, and animal cells and mammals with a targeted disruption of an animal cells and mammals with a targeted disruption of an canimal cells modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with costeoregulin activity. The modulators of activity may be useful in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification
  OOM1 is useful as an immunogen to produce antibodies agains vitro assays to screen for agents or drugs, which modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin -
                                                                                                                                                                                                                                          Gape
                                                       osteomalacia-related protein-1 (00M-1).

Note: The present sequence states that this sequence is encoded by DNA sequence shown in SEQ ID NO: 1 (AAD21889) of the specification However this does not appear to be the case.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; bone; homeostasis; adipose; calcification; is; osteoporosis; osteopathic; antiarteriosclerotic;
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                     Length 525;
population. OOM1 is useful as an immunogen to produce antium OOM1 and in vitro assays to screen for agents or drugs, whis cellular processes. The present sequence is human oncogenic
                                                                                                                                                                                                                                        Indela
                                                                                                                                                                                                 Score 126; DB 23;
Pred. No. 7.3e-11;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hames LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human osteoregulin (mature polypeptide)
                                                                                                                                                                                                                                                                                                      242 TDLOERGDNDISPFSGDGQPFKD 264
                                                                                                                                                                                                                                                                             1 TDLOERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                       AAB82923 standard; Protein; 540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 59-61; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gowen LC,
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-FEB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2001; 2001EP-0301768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                 l Similarity 100.
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-604111/69.
                                                                                                                                                              525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoregulin; humatherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH26811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1130098-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB82923;
                                                                                                                                                                Sequence
                                                                                                                                                                                                   Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy.
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                      AAB8292
```

```
RESULT 14
                                                                                                                                                                                                    AAU93703
88866666
                                                                                                                                                       g
                                                                                                                                                                                                                        ð
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of human osteoregulin, a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. The sequence is predicted from the nucleother of number of sequence (see AAH26809) of isolated osteoblast cDNA. A splice variant of human osteoregulin was also identified (see AAB8220). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, antibodies, host cells which express heterologous osteoregulins, and animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with osteoregulin activity. The modulators of activity may be useful
                                                                              Gaps
                                                                                                                                                                                                                                                                   Osteoregulin, human, bone, homeostasis, adipose, calcification, atherosclerosis, osteoporosis, osteopathic, antiarteriosclerotic,
                                                                            0
                                                      Length 540;
preventing osteoporosis, and for
                                                                            Indels
                                                       DB 22;
                                                                             ö
                                                     100.0%; Score 126; DB 22;
100.0%; Pred. No. 7.6e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hames LM;
(claimed), for treating and preventing os stimulating bone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by TCA"
                                                                                                                                                                                                                                                                                                                                                  ...37
'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                     38..556
/label= Mature_protein
                                                                                                                      257 TDLOERGDNDISPFSGDGOPFKD 279
                                                                                                  23
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                             AAB82921 standard; Protein; 556 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 48-49; 90pp; English
                                                                                                  1 TDLQERGDNDISPFSGDGQPFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gowen LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-FEB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2001; 2001EP-0301768
                                                                                                                                                                                                                          (first entry)
                                                      Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-604111/69.
                                                                                                                                                                                                                                                Human osteoregulin.
                                 540 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH26809
                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            EP1130098-A2
                                                                                                                                                                                                                          21-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown TA,
                                                                                                                                                                                                    AAB82921;
                                  Sequence
                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                           therapy
                                                                                                                                                       RESULT 13
                                                                                                                                                                   AAB8292
                                                                                                                                                                                         ប្បង្គន្ល
                                                                                                  ò
                                                                                                                     요
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of esteoblast or dontoblast cells on the surface of the new skeletal growth. AAU93081-AAU93126 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif
                                                                                                                                                                                                                                                                             Gaps
mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification (claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                     Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 40;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                  100.0%; Score 126; DB 22;
100.0%; Pred. No. 7.8e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth enhancing peptide #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 23;
Pred. No. 2.8e-08;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                              273 TDLQERGDNDISPFSGDGQPFKD 295
                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.2%; Sc._
100.0%; Pre
                                                                                                                                                                                                                                                                                                                               1 TDLQERGDNDISPFSGDGQPFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumagai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 20; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU93703 standard; peptide; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001; 2001WO-US25101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2000; 2000US-225879P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 RGDNDISPFSGDGQPFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                              Local Similarity 100.
les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIGB-) BIG BEAR BIO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    foneda T, Nomizu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dental product bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-329525/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                   556 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200213775-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU93703;
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
硆
```

```
The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts of steaclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a protein of a matrix extracellular phosphoglycoprotein containing an RGD motif of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; weakness; matrix excracellular phosphoglycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein of matrix extracellular phosphoglycoprotein containing RGD #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 12; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kumagai Y, Blacher RW, Yoneda T;
                                                                                                                                                                                                      AAO20353 standard; protein; 40 AA.
1 RGDNDISPFSGDGQPFKD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001WO-US25542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-2000; 2000US-0641034.
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIGB-) BIG BEAR BIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-291971/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200214360-A1
                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                        AA020353;
                                                                                                                    AAO20353
AAO20
```

80.2%; Score 101; DB 23; Length 40; 100.0%; Pred. No. 2.8e-08; 0; Indels 100.0%; Prec. ... 6 RGDNDISPFSGDGQPFKD 23 18; Conservative Best Local Similarity Matches 18; Conserv ò

Query Match

ö

Gaps

ö

RGDNDISPFSGDGQPFKD 18

쉽

Search completed: January 29, 2004, 12:38:35 Job time : 43.9737 secs

THIS PAGE BLANK (USPTO)

Appli Appli Appli Appli Appli Appli Appli

US-08-330-978-1 US-08-474-042-1 US-08-744-558-1 US-08-774-592-1 US-08-295-411-3 PCT-US92-10068-1 PCT-US92-10042-3

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence 1, Appli Sequence 31826, A

US-09-241-333-1 US-09-252-991A-31826

ALIGNMENTS

US-09-367-777-44 US-09-367-791A-27 US-08-990-114-1

Sequence Sequence Sequence

Appl Appli

Sequence

-252-991A-19718

```
GENERAL INFORMATION:
APPLICANT: Fischbarg, Jorge
APPLICANT: Czegledy, Ferenc
APPLICANT: Legicaly, Ferenc
APPLICANT: Lerovich, Pavel
APPLICANT: Li, Jun
APPLICANT: Li, Jun
APPLICANT: Cheung, Min
ITILE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
ITILE OF INVENTION: A METHOD FOR PROTEIN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISP PPC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,844
FILING DATE: 14-DEC-1994
CLLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Tang, Henry Y.S.
REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: 28,705
REFERENCE/DOCKET NUMBER: 22,705
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATRADEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
CCATION: 1..301
CTHER INFORMATION: Porin protein
US-08-355-844-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rhodobacter capsulatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/08355844
; Patent No. 5940307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: N'
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-355-844-2
   Sequence 2, Appli
Sequence 3614, Ap
Sequence 405, Appl
Sequence 405, Appl
Sequence 31834, A
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4, Appl
2899, A
1, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32044, A
7703, Ap
2, Appli
2, Appli
6, Appli
7, Appli
8, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                    January 29, 2004, 12:37:19 ; Search time 17.5526 Seconds (without alignments) 55.442 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3 Sequence 3 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 6 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6
Sequence 6
Sequence 6
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6
Sequence 6
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lssued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-134-001C-3614

US-09-139-677A-405

US-09-252-991A-31834

US-08-341-843B-9

US-08-427-497E-14

US-08-252-991A-22099

US-09-328-352-7703

US-09-328-352-7703

US-08-176-126B-2

US-08-176-126B-2

US-08-176-126B-2

US-08-176-126B-2

US-08-18-350-441-2

US-08-493-6

US-08-493-6

US-08-493-6

US-08-493-6

US-08-493-6

US-08-493-6

US-08-493-6

US-08-463-816-6

US-08-463-816-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-812-485A-49
126
1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect acore:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
No.
                                                                                                                                                                                                                                                           Run on:
```

```
US-09-134-001C-3614
US-09-134-001C-3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-199-637A-405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                         ö
                                                         Gaps
                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                Query Match
41.3%; Score 52; DB 2; Length 301;
Best Local Similarity 58.8%; Pred. No. 3.6;
Matches 10; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                        APPLICANT: Fischbarg, Jorge
APPLICANT: Czegledy, Ferenc
APPLICANT: Czegledy, Ferenc
APPLICANT: Liserovich, Pavel
APPLICANT: Li, Jun
APPLICANT: Cheung, Min
TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
TITLE OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Brumbaugh, Graves, Donohue & Raymond
30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 41.3%; Score 52; DB 5; Similarity 58.8%; Pred. No. 3.6; 10; Conservative 2; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A29927-50/29910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNDMER:
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Tang, Henry Y.S.
REGISTATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A29927-50/;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1.301
; OTHER INFORMATION: Porin protein
PCT-US95-16126-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodobacter capsulatue
                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9516126 GENERAL INFORMATION:
                                                                                                                                     92 TDLDDRGGNDIPYLTGD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 TDLDDRGGNDIPYLTGD 108
                                                                                                1 TDLQERGDNDISPFSGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TDLQERGDNDISPFSGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 301 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                     PCT-US95-16126-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                 g
                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
```

RESULT, 3

```
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-07
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3614
LENGTH: 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Trendals, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/36/1002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR APPLICATION NUMBER: 997-11-25
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 405
LENGTH: 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.3%; Score 47; DB 4; ilarity 52.4%; Pred. No. 99; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.3%; Score 47; 58.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-31834
; Sequence 31834, Application US/09252991A
; Partent No. 6551705;
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
Sequence 3614, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-199-637A-405
; Sequence 405, Application US/09199637A
; Patent NO. 6355411
; Patent INFORMATION:
; APPLICANT: Ausubel, Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ausubel, Frederick
Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 TDLRPSIDNDLKPFMAYKSGD 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TDLQERGDNDISPF----SGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 ĠĎEĎQLPSVĠPĠQVFKĎ 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 GDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.1%; Score 45.5; DB 2; Length 96; Best Local Similarity 61.1%; Pred. No. 9.4; Matches 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-427-497E-14

Sequence 14, Application US/08427497E

Sequence 14, Application US/08427497E

Sequence 14, Application US/08427497E

Settle No. 1896124

TITLE OF INVENTION: A Method for Characterizing the TITLE OF INVENTION: Nucleotide Sequence of LICAM and TITLE OF INVENTION: the Nucleotide Sequence TITLE OF INVENTION: Characterized Thereby NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
MOLECULE TYPE: amino acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGIAAL SOURCE:
ORGANISM: mouse
INDIVIDUAL ISOLATE: 8 day old mouse brain
IMBEDIATE SOURCE:
LIBBARX: lamda GT 10 and lamda GT11
LIBBARX: lamda GT 10 and lamda GT11
LIDBARX: lamda GT 10 and lamda GT11
LIDBARX: sources of several clones
PUBLICATION INFORMATION:
AUTHORS: Tacke, R.
AUTHORS: Scherzer, H.
AUTHORS: Schachner, M.
AUTHORS: Schachner, M.
TITLE: member of the immunoglobulin
TITLE: member of the immunoglobulin
TITLE: superfamily with binding domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.50 inch, 720 KD MEDIUM TYPE: Storable COMPUTER: Compaq Prolines 5100e OPERATING SYSTEM: DOS 5.0 SOFTWARE: ASCII CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/427,497E FILING DATE: April 24, 1995 CLASSIFICATION: 435 PRIOR APPLICATION UMBER: 07/904,991 FILING DATE: June 26, 1992 ATTORNEY/AGENT INFORMATION: NAME: Minner, Nichard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee STREET: 1100 Superior Avenue STREET: Suite 700 CITY: Cleveland STATE: Ohio COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to fibronectin
: NATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 DLQERGDNDISPESGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 DLQERGDSD-KYFIEDGK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 24,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701-703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE: member
TITLE: super!
TITLE: simil:
JOURNAL: NATH
VOLUME: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-341-843B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
             NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.5%; Score 46; DB 4; Length 425; Best Local Similarity 56.2%; Pred. No. 43; Matches 9; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEREALL INTOCRMATION:

APPLICANT: Lemmon, Vance
TITLE OF INVENTION: A Method for Characterizing the
TITLE OF INVENTION: Nucleotide Sequence of LICAM and
TITLE OF INVENTION: Characterized Thereby
TITLE OF INVENTION: Characterized Thereby
NUMBER OF SUCUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Fay, Sharpe, Beall, Fagan,
ADDRESSEE: Minnich & McKee
STREET: Suite 700
CITY: Chio
CONFUTER: Objection Avenue
STREET: Suite 700
CITY: Chio
COMPUTER: Chio
COMPUTER: Company Prolinea 5100e
OOMPUTER: Company Prolinea 5100e
OOMPUTER: ASTATE
COMPUTER: ASTATE
COMPUTER
COMPUTER: ASTATE
COMPUTER
COMPUTER: ASTATE
COMPUTER
COMPUTER: ASTATE
COMPUTER
COMPU
      TITLE OF INVENTION: NUCLEIC ACID AND AMINO AV
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-341-843B-9; Sequence 9, Application US/08341843B; Patent No. 5872225; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (216) 861-5582
TELEFAX: (216) 241.1666
TELEEX: (216) 980162
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ERGDNDISPFSGDGQP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 EQGRNDASESTGGGQP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
```

ઠે 셤 ï

```
Sequence 32044, Application US/09252991A
Sequence 32044, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MARC J.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR SPUICH DATE: 1998-02-18
PRIOR SPUICH DATE: 1998-02-18
PRIOR SPUICH DATE: 1998-02-18
PRIOR SPUICH DATE: 1998-02-18
                                                                                                                                                                         Sequence 21, Application US/08506296B
Patent No. 6313265
GENERAL INFORMATION
GENERAL INFORMATION: GREG
APPLICANT: Cunningham, Bruce A. APPLICANT: Cunningham, Bruce A. TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE ITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE CORRESPONDENCE ADDRESS:
ADDRESSEE: The SCRIPPS Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45.5; DB 4; Length 1260;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA: US/08/506,296B
FILING DATE: 24-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92037
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
8 DNDISPFSGD-----GQPF 21
                                                   17 DGELKPFSGDTDIFIYPGRPF 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    558 DLÓERGDSD-KYFIEDGK 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DLQERGDNDISPFSGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Fiting, Thomas
REGISTRATION NUMBER: 34,162
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 554-2937
TELEPAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-506-2968-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 10550 No. 6
CITY: La Jolla
STATE: California
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-32044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino TOPOLOGY: li
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25899, Application US/09252991A

| Sequence 25899, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
| CURRENT APPLICATION NUMBER: US 60/074,788
| PRIOR APPLICATION NUMBER: US 60/074,788
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR PILING DATE: 1998-02-18
| NUMBER OF SEQ ID NOS: 33142
| LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.1%; Score 45.5; DB 4; Length 101; Best Local Similarity 42.9%; Pred. No. 9.9; Matches 9; Conservative 3; Mismatches 2; Indels "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: mouse
INDIVIDUAL ISOLATE: 8 day old mouse brain
IMMEDIATE SOURCE:
LIBRARY: lamda GT 10 and lamda GT11
CLONE: synthesis of several clones
PUBLICATION INFORMATION:
AUTHORS: Moos, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE: Neural adhesion molecule L1 is a TITLE: member of the immunoglobulin TITLE: superfamily with binding domains TITLE: similar to fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45.5; C
Pred. No. 9.4;
2; Mismatches
     CWR 2 149-3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT CORGANISM: Pseudomonas aeruginosa US-09-252-991A-22899
                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DLQERGDNDISPFSGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDENDESS: aingle
STRANDENDESS: aingle
TOPOLOGY: linear
MOLECULE TYPE: amino acids
HYPOTHETICAL: irrelevant
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.1%;
61.1%;
     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fruh, K.
Schachner, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tacke, R.
Scherer, H.
Teplow, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           701-703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL: NA'
VOLUME: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-427-497E-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
```

ద

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dawson, Paul A.
TITLE OF INVENTION: ILEAL BILE ACID TRANSPORTER COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%; Score 44; DB 2; Length 348; 53.3%; Pred. No. 68;
                                                                                                                                                                                 34.9%; Score 44; DB 1; Length 348;
53.3%; Pred. No. 68;
tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAPPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,435
FLING DATE: 26-JUN-1996
CLASSIFICATION NUMBER: US/08/669,435
FILING DATE: 29-DEC-1993
CLASSIFICATION NUMBER: US/08/176,126
FILING DATE: 29-DEC-1993
CLASSIFICATION:
ATTORNEY/AGENT INO:
NAME: Parker, David L.
REGISTRATION NUMBER: 32.165
REFERENCE/DOCKET NUMBER: 32.165
REFERENCE/DOCKET NUMBER: WAKE:002/PAR
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08669435
Patent No. 5869265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|||: ||: | |
320 TELQEKTDNEMEPRS 334
                                                                                                                                                                                                                                                                                         |:|||: ||: | |
320 TELQEKTDNEMEPRS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TDLQERGDNDISPFS 15
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                    1 TDLQERGDNDISPFS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: na INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 348 amino acida TYPE: amino acid
                                                                                                                                                                  Query Match
Best Local Similarity 53.3%
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                    MOLECULE TYPE: protein US-08-176-126B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                         US-08-669-435-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                              Section 7703, Application US/09328352
Section 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08176126B
Fatent No. 5589358
GENERAL INFORMATION:
APPLICANT: Dawnen, Paul A.
TITLE OF INVENTION: METHODS
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                 4
                                                                                                    Score 45; DB 4; Length 547;
Pred. No. 81;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.9%; Score 44; DB 4; Length 186; 38.1%; Pred. No. 33; tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER, KEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/176,126B
FILING DATE: 29-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: WAKE:002/PAR
TELECHONE: (512) 418-3000
                                                                                                                                                                                                              11 EADEVGDDDLVPGAGNRQELGQPLHD 436
                                                                                                                                                                                     2 DLQERGDNDISPFSGD----GQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7703
                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                    Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (512) 418-3000
(512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 38.1<sup>1</sup>
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
STATE: Texas
                                                              US-09-252-991A-32044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 77210
                                                                                                                                                                                                                                                                                     RESULT 11
US-09-328-352-7703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7703
LENGTH: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-176-126B-2
    LENGTH: 547
TYPE: PRT
                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
LENGTH: 475 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 DISPFSGDGOPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 DDSPFCQDGSPFQN 92
                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                            ;
TOPOLOGY:
US-08-278-091-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                     TITLE OF INVENTION: ILEAL BILE ACID TRANSPORTER COMPOSITIONS NUMBER OF SEQUENCES: 11
CORRESSONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 5; Length 348;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                         STATE: TEXAS
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/176,126
FILING DATE: 29-DEC-1993
CLASSIFICATION:
CLASSIFICATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: WAKEO05P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (112) 418-3000
TELEPHONE: (112) 418-3000
TELEPRA: 79-0924 (1) GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14431A
FILING DATE: 29-DEC-1994
CLASSIFICATION:
              Sequence 2, Application PC/TUS9414431A GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-278-091-6
'Sequence 6, Application US/08278091
'Patent No. 5506139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOOSMORE, Sheena M
YANG, Yan-Ping
CHONG, Pele
COMEN, Raymond P.
KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|||: ||: | |
320 TELQEKTDNEMEPRS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TDLQERGDNDISPFS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.9
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LOOSMC
PCT-US94-14431A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US94-14431A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
```

TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:

APPLICANT: APPLICANT: APPLICANT: APPLICANT: E: Sim & McBurney Suite 701, 330 University Avenue

ADDRESSEE: Sim & STREET: Suite 701 CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: MSG 1R7

COMPUTER READABLE FORM:

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                         CURRAILING SISIEM:
COFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,091
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-371
TELEFONNICATION INFORMATION:
TELEFONNICATION INFORMATION:
TELEFAX: (416) 595-1153
TELEFAX: (416) 595-1163
THOORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.9%; Score 44; DB 1; Best Local Similarity 57.1%; Pred. No. 97; Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 29, 2004, 12:41:37
Job time : 17.5526 secs
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

3, Appli 7, Appli 12, Appl 23, Appl 13, Appl 6, Appli

Sequence 23,

Sequence 1 Sequence 6 Sequence 4

Appl

Sequence 30, Sequence 47, Sequence 10, Sequence 2, R Sequence 2, R Sequence 4, R

US-10-360-202-1 US-10-360-202-3 US-10-360-202-3 US-10-360-202-3 US-10-360-202-12 US-09-812-485A-23 US-09-812-485A-48 US-09-812-485A-47 US-09-812-485A-47 US-09-812-485A-47 US-10-360-202-10 US-10-360-202-10 US-10-360-202-15 US-09-812-485A-25 US-09-812-485A-25 US-09-812-485A-25 US-09-812-485A-25 US-09-812-485A-25 US-09-812-485A-25 US-09-812-485A-25 US-09-812-485A-25 US-09-812-485A-25 US-09-812-485A-27 US-09-814-550-5

Appl Applit Appl

Sequence Sequence Sequence Sequence

Sequence 32,

Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence

ALIGNMENTS

Sequence

```
US-09-812-485A-49

i Sequence 49, Application US/09812485A

i Sequence 49, Application US/09812485A

i Publication No. US20020197267A1

i GENERAL INFORMATION:

APPLICANT: Kumagai, Yoshinari

APPLICANT: Yoneda Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing

TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases

TITLE OF INVENTION WINBER: US/09/812,485A

TITLE NEFERENCE: BEAR-006C1P

FILE REFERENCE: BEAR-006C1P

PRIOR APPLICATION NUMBER: US/09/41,034

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 50

SOGTWARR: PastSEQ for Windows Version 4.0

SEQ ID NO 49

LENGTH: 23

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

ORGANISM: Artificial Sequence

FEATURE:

ORGANISM: ARIDATION

US-09-812-485A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDLOERGDNDISPFSGDGQPFKD 23
RESULT 2
US-10-360-202-1
1005
1005
1005
1001
1001
886
886
887
881
881
881
79
                                                                                                                                                                                                                                                          68
66
57
57
52
53
54
59
59
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49, Appli
Sequence 17, Appli
Sequence 17, Appl
Sequence 18, Appl
Sequence 34, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 8, Appli
                                                                                 January 29, 2004, 12:38:39; Search time 32.6842 Seconds (without alignments) 146.247 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

| cgn2_6/ptodata/l/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/l/pubpaa/PCT_NEW_PUB_pep:*
3: /cgn2_6/ptodata/l/pubpaa/USO6_NEW_PUB_pep:*
4: /cgn2_6/ptodata/l/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/l/pubpaa/USO6_NEW_PUB_pep:*
6: /cgn2_6/ptodata/l/pubpaa/USO6_NEW_PUB_pep:*
7: /cgn2_6/ptodata/l/pubpaa/USO8_NEW_PUB_pep:*
8: /cgn2_6/ptodata/l/pubpaa/USO8_NEW_PUB_pep:*
9: /cgn2_6/ptodata/l/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/l/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/l/pubpaa/USO9C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/l/pubpaa/USO9C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/l/pubpaa/USO9C_PUBCOMB.pep:*
14: /cgn2_6/ptodata/l/pubpaa/USOOC_PUBCOMB.pep:*
15: /cgn2_6/ptodata/l/pubpaa/USOOC_PUBCOMB.pep:*
16: /cgn2_6/ptodata/l/pubpaa/USOOC_PUBCOMB.pep:*
16: /cgn2_6/ptodata/l/pubpaa/USOOC_PUBCOMB.pep:*
17: /cgn2_6/ptodata/l/pubpaa/USOOC_PUBCOMB.pep:*
18: /cgn2_6/ptodata/l/pubpaa/USOOC_PUBCOMB.pep:*
18: /cgn2_6/ptodata/l/pubpaa/USOOC_PUBCOMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-812-485A-49
US-10-360-202-11
US-10-360-202-117
US-10-360-202-18
US-09-812-485A-117
US-09-814-422-34
US-09-794-422-6
Z US-09-794-422-46
Z US-09-794-422-46
Z US-09-794-422-8
Z US-09-794-422-8
Z US-09-794-422-8
Z US-09-794-422-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-360-202-6
US-10-360-202-2
US-10-360-202-8
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      789580 segs, 207824079 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                               US-09-812-485A-49
126
1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                Perfect acore:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
```

ö

Gaps

ö

Length 23; Indele

```
Sequence 1, Application US/09812485A
Publication No. US20020197267A1
Publication No. US20020197267A1
Publication No. US20020197267A1
REBERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Kumagai, Yoshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Integrin Binding Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR FILING DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 97;
                                       APPLICANT: OKANO, TOSHIO
APPLICANT: TSUGAWA, NAOKO
APPLICANT: TSUGAWA, NAOKO
APPLICANT: TSUGAWA, NAOKO
APPLICANT: Blacher, Russell W
APPLICANT: Kumagai, Yoshinari
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OP VITAMIN D DEFICIENCY
TITLE OF INVENTION: OP VITAMIN D DEFICIENCY
TITLE OF INVENTION: OP VITAMIN D DEFICIENCY
CURRENT APPLICATION NUMBER: US/10/360,202
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,548
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 126; DB 10; Best Local Similarity 100.0%; Pred. No. 8.1e-12; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 126; DB 12;
Pred. No. 1.7e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Synthetic oligopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: peptidic compound US-09-812-485A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 rolóskabnolsPrsabagerko 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDLQERGDNDISPFSGDGQPFKD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/09794422
Publication No. US20030166239A1
GENERAL INFORMATION:
APPLICANT: Brown, Thomas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 23; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
    Publication No. US20030186891A1
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-794-422-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-360-202-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-812-485A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tsugawa, Naoko
APPLICANT: Tsugawa, Naoko
APPLICANT: Tsugawa, Naoko
APPLICANT: Nakagawa, Kinie
APPLICANT: Blacher, Rusesll W
APPLICANT: Kunagai, Yoshinari
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: COMPOSITION DEFICIENCY
FILE REPRENCE: BEAR-010
CURRENT APPLICATION NUMBER: US/10/360,202
CURRENT FILING DATE: 2003-02-07
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 126; DB 12;
100.0%; Pred. No. 1.6e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 126; DB 12;
100.0%; Pred. No. 1.7e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Synthetic oligopeptide US-10-360-202-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic oligopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TDLOERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TDLÓERGDNDISPESGDGOPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDLOERGDNDISPFSGDGOPFKD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-360-202-18
.; Sequence 18, Application US/10360202
Sequence 1, Application US/10360202
Publication No. US20030186891A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-360-202-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
```

g

ò

ö

Gaps

ö

ö

Gaps

.; 0

Matches

à 셤

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1. Application US/10311840

Publication No. US20030175808A1

GENERAL INFORMATION:

APPLICANT: KURCKAMA, Tomofumi

APPLICANT: WORIMOTO, Shigeto

TITLE OF INVENTION: No. US20030175808A1e1 Protein and its DNA
FILE REFERENCE: 2738USOR

CURRENT APPLICATION: No. US20030175808A1e1 Protein and its DNA
FILE REFERENCE: 2738USOR

CURRENT APPLICATION NUMBER: US/10/311,840

CURRENT FILING DATE: 2002-12-18

PRIOR PLICATION NUMBER: JP 2000-191088

PRIOR FILING DATE: 2001-06-20

PRIOR FILING DATE: 2000-06-21

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 1

LINGTH: 525
                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                   Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                   Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 126; DB 12;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 126; DB 12;
100.0%; Pred. No. 5.5e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OS-09-794-42-2-9
SQUEGREE 46, Application US/09794422
Publication No. US20030166239A1
GENERAL INFORMATION:
APPLICANT: Brown, Thomas A.
APPLICANT: De Wet, Jeffrey R.
APPLICANT: Gowen, Lori C.
TITLE OF INVENTION: Mammalian Osteoregulins
FILE REFERENCE: PC10445
CURRENT APPLICATION 'NUMBER: US/09/794,422
CURRENT APPLICATION 'NUMBER: 60/185,617
PRIOR APPLICATION NUMBER: 60/185,617
PRIOR PILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalian Osteoregulins
                          CURRENT APPLICATION NUMBER: US/09/794,422
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,617
PRIOR PILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/234,500
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 6
LENGTH: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 TDLQERGDNDISPFSGDGQPFKD 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 TDLOERGDNDISPFSGDGOPFKD 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100:
Matches 23; Conservative
         PC10445
                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-794-422-46
                                                                                                                                                                                                                                                                                                          US-09-794-422-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-311-840-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09814550
Sequence 2, Application US/09814550
Patent No. US20020102641A1
GENERAL INFORMATION:
APPLICANT: Schiau', Susan
APPLICANT: Madden, Stephen
APPLICANT: Manavalan, Parthasarathy
APPLICANT: Levine, Michael
APPLICANT: Jan de Beur, Suzanne
TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1
FILE REFERENCE: 5014US
CURRENT FILING DATE: 2001-03-22
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2
LENGTH: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   , DB 12;
5.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 126; DB 10; Best Local Similarity 100.0%; Pred. No. 5.5e-11; Matches 23; Conservative 0; Mismatches 0;
APPLICANT: De Wet, Jeffrey R.
APPLICANT: Gowen, Lori C.
APPLICANT: Gowen, Lori C.
TITLE OF INVENTION: Mammalian Osteoregulins
FILE REFERENCE: PC10445
CURRENT APPLICATION NUMBER: US/09/794,422
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 2000-02-29
PRIOR PLING DATE: 2000-02-29
PRIOR PLING DATE: 2000-02-20
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 126; D
Best Local Similarity 100.0%; Pred. No. 5.3
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalian Osteoregulins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 TDLQERGDNDISPFSGDGQPFKD 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 TDLQERGDNDISPFSGDGQPFKD 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TOLOERGDNDISPESGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09794422
Publication No. US20030166239A1
GENERAL INFORMATION:
APPLICANT: Brown, Thomas A.
APPLICANT: De Wet, Jeffrey R.
APPLICANT: Gowen, Lori C.
APPLICANT: Hames, Lynn M.
TITLE OF INVENTION: Mammalian Osteoz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-794-422-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-09-794-422-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-814-550-2
```

g ò

```
TYPE: PRT
ORGANISM: Artificial sequence
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-360-202-2
                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                      Query Match 100.0%; Score 126; DB 12; Length 540; Best Local Similarity 100.0%; Pred. No. 5.7e-11; Matches 23; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10360202

Sequence 4, Application US/10360202

Publication No. US20030186891A1

GENERAL INFORMATION:

APPLICANT: Okano, Toshio

APPLICANT: Blacher, Russell W

APPLICANT: Blacher, Russell W

APPLICANT: Wanagaa', Yoshinari

TITLE OF INVENTION: COPPOSITIONS AND METHODS FOR TREATMENT

TITLE OF INVENTION: OF VITAMIN D DEFICIENCY

FILE REFERENCE: BEAR-010

CURRENT APPLICATION NUMBER: US/10/360,202

CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: 60/335,548

PRIOR APPLICATION NUMBER: 60/335,548

WUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 126; DB 12;
100.0%; Pred. No. 5.9e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09794422
; Sequence 8, Application US/09794422
; Publication No. US20030166239A1
GENERAL INFORMATION:
APPLICANT: Brown, Thomas A.
APPLICANT: Gowen, Lori C.
APPLICANT: Hames, Lynn M.
TITLE OF INVENTION: Mammalian Osteoregulins
FILE REFERENCE: PC10445
CURRENT APPLICATION NUMBER: US/09/794,422
CURRENT APPLICATION NUMBER: 050/185,617
PRIOR APPLICATION NUMBER: 60/185,617
PRIOR APPLICATION NUMBER: 2000-02-29
PRIOR APPLICATION NUMBER: 60/234,500
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; LENGTH: 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 TDLQERGDNDISPFSGDGQPFKD 295
                                                                                                                                                                                                                                                                                                                 257 TDLQERGDNDISPFSGDGQPFKD 279
                                                                                                                                                                                                                                                                                    1 TDLQERGDNDISPFSGDGQPFKD 23
                            PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100..
Best Local 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-794-422-8
                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
       NUMBER OF SEQ ID NOS:
                                                                                                                                             US-09-794-422-46
                          SOFTWARE: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 23
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
```

```
ö
                                                                                                                                                    Gaps
                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TUBURAN NAONO
APPLICANT: Nakagawa, Naono
APPLICANT: Nakagawa, Kimie
APPLICANT: Blacher, Russell W
APPLICANT: Runagai, Yoshinari
ITILE OF INVENTION: OF VITAMIN D DEFICIENCY
FILE REPERENCE: BEAR-010
CURRENT APPLICATION NUMBER: US/10/360,202
CURRENT APPLICATION NUMBER: 60/335,548
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Okano, Toshio
APPLICANT: Ckano, Naoko
APPLICANT: Tsugawa, Naoko
APPLICANT: Nakagawa, Kimie
APPLICANT: Blacher, Russell W
APPLICANT: Kumagai, Yoshinari
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
ITILE OF INVENTION: OF VITAMIN D DEFICIENCY
ITILE OF INVENTION: OF VITAMIN D DEFICIENCY
ITILE OF INVENTION: OF VITAMIN D DEFICIENCY
CURRENT FILIAG DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,548
PRIOR PILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO :
                                                                                       Query Match 97.6%; Score 123; DB 12; Length 23; Best Local Similarity 95.7%; Pred. No. 4.6e-12; Matches 22; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.3%; Score 115; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 7e-11;
Matches 21; Conservative 0; Mismatches 0; Indels
; OTHER INFORMATION: Synthetic oligopeptide US-10-360-202-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide
US-10-360-202-6
                                                                                                                                                                                                         1 TDLOERGDNDISPFSGDGOPFKD 23
                                                                                                                                                                                                                                                             1 TDLOERGDNDMSPFSGDGOPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TDLQERGDNDISPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TDLÓERGDNDISPFSGDGÓPF 21
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10360202
Publication No. US20030186891A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10360202
Publication No. US20030186891A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-10-360-202-8

i) Sequence 8, Application US/10360202

i) Publication No. US20030186691A1

i) GENERAL INPORMATION:

i) APPLICANT: Okano, Toshio

i) APPLICANT: Nakagawa, Kimie

i) APPLICANT: Nakagawa, Kimie

i) APPLICANT: Runagai, Yoshinari

i) TITLE OF INVENTION: OF VITAMIN D DEFICIENCY

i) CURRENT FILING DATE: 2003-02-07

i) PRIOR FILING DATE: 2003-02-07

i) PRIOR FILING DATE: 2003-02-07

i) PRIOR FILING DATE: 2003-02-08

i) NUMBER OF SEQ ID NOS: 23

i) SCO ID NO 8

i ENGCTH: 20

i) TYPE: PRT

i) ORDANISM: Artificial sequence

i) FRATURE:

i) OTHER INFORMATION: Synthetic oligopeptide

US-10-360-202-8
                                                                                                         Query Match 88.9%; Score 112; DB 12; Length 23; Best Local Similarity 91.3%; Pred. No. 2.2e-10; Matches 21; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.3%; Score 110; DB 12; Length 20; Best Local Similarity 100.0%; Pred. No. 3.9e-10; Matches 20; Conservative 0; Mismatches 0; Indels
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide
US-10-360-202-2
                                                                                                                                                                                                                     1 TDLQERGDNDISPFSGDGOPFKD 23
                                                                                                                                                                                                                                                    1 TDLQERDGNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DLOERGDNDISPFSGDGOPF 21
                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

Search completed: January 29, 2004, 12:42:44 Job time : 33.6842 secs

1 DLQERGDNDISPFSGDGQPF 20

g

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

January 29, 2004, 12:36:28; Search time 16.3421 Seconds (without alignments) 135.349 Million cell updates/sec Run on:

US-09-812-485A-49 126 1 TDLQERGDNDISPFSGDGQPFKD 23 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\* Database :

summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOFTWANTES	
Result No.	Score		Query Match Length	DB	ID	Description
-	52	41.3	301	7	S16070	porin - Rhodobacte
7	52	41.3	320	~	JC5727	ď
٣	49.5	39.3	1259	~	S36126	neural cell adhesi
4	48	38.1	277	7	AD3322	lysozyme (EC 3.2.1
'n		38.1	385	~	D72858	late expression fa
œ	48	38.1	385	~	T41811	orf67 -
7	47	37.3	444	~	B83891	intracellular alka
8	47	37.3	481	~	AH0410	global stress requ
σ	47	37.3	825	~	B89944	eti
10	46.5	•			S38783	
11	46.5	•			161186	alpha-7 integrin -
12	46.5	36.9	1137		JC5950	integrin alpha-7 c
13	46		308	~	AD3154	nucleotidyltransfe
14	46	36.5	365		E98133	hypothetical prote
15	45.5	36.1	347		A83170	S-adenosylmethioni
16	•	36.1			S05479	neural cell adhesi
17	45	35.7			AI1365	a probable repress
18	45	35.7			C84856	probable protein k
19	45	35.7	393		S59499	cellulase egl1 - s
20	45	35.7	472		JQ0802	levansucrase (EC 2
21	45	35.7	851		T38173	probable phosphati
22	45	35.7	913		D82885	
23	44.5	35.3	698		D65210	yjbH protein precu
24	44.5		698		D91255	
25	44.5	35.3	698		H86095	
26	44	34.9			A49876	u
27		34.9			S15337	heat shock protein
28	44	•	475	N	AC0528	protease DO precur
53	44	34.9	ø	~	D83511	flagellar hook-ass

probable L2 riboso	ribosomal protein	cobT protein - Pae	integrin alpha-5 c	integrin alpha cha	integrin alpha cha	En/Spm-like transp	hypothetical prote	conserved hypothet	probable transmemb	transcription init	RNA polymerase sig	RNA polymerase sig	hypothetical prote	xanthine dehydroge	hypothetical prote
C71507	A81661	D38162	844250	T09403	T09433	G84608	F90274	G72258	T39285	RNAGVS	AF2842	G97619	E87592	G87573	E96590
N	~	~	~	~	N	~	~	7	7	-	~	~	~	~	7
284	284	631	1053	1115	1115	140	300	335	629	684	684	684	762	779	891
'n	r.	'n	ĸ,	'n	'n	۲.	٦.	٦.	۲.	۲.	۲.	٦.	۲.	٦.	٦.
34	34	34	34	34	34	34	34	34	34	34.1	34	34	34	34	34
43.5	43.5	43.5	43.5	43.5	43.5	43	43	43.	43	43	43	43	43	43	43
0	_	~	m	4	'n	g	7	<b>6</b> 0	σ		-	~		4	LO.

## ALIGNMENTS

21-Jul-199			0; Сарв
RESULT 1 S16070 porin - Rhodobacter capsulatus C;Species: Rhodobacter capsulatus C;Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995 C;Accession: S16070	R;Schiltz, E.; Kreusch, A.; Nestel, U.; Schulz, G.E. Eur. J. Biochem. 199, 587-594, 1991 A;Title: Primary structure of porin from Rhodobacter capsulatus. A;Reference number: S16070; MUID:91330909; PMID:1651239 A;Accession: S16070	A.Status: preliminary A.Molecule type: protein A.Residues: 1-301 «EUR» A.Experimental source: strain 37b4 A.Note: the source is designated as Rhodobacter capsulatus	Query Match 41.3%; Score 52; DB 2; Length 301; Best Local Similarity 58.8%; Pred. No. 3.1; Matches 10; Conservative 2; Mismatches 5; Indels

92 TDLDDRGGNDIPYLTGD 108 1 TDLQERGDNDISPFSGD 17 ઠે

ô

g

porin precursor - Rhodobacter capsulatus
C;Species: Nate: 09-05c-1997 #sequence\_revision 23-Jan-1998 #text\_change 07-May-1999
C;Accession: JG527; PC4414
R;Trieschmann, M.D.A.; Pattus, F.; Tadros, M.H.
Gene 183, 61-68, 1996
A;Trieschmann, M.D.A.; Pattus, F.; Tadros, M.H.
Gene 183, 61-68, 1996
A;Trieschmann, M.D.A.; Pattus, F.; Tadros, M.H.
A;Reference number: JG5727; MUID:97149280; PMID:8996088
A;Reference number: JG5727; MUID:97149280; PMID:8996088
A;Recession: JG5727; MUID:97149280; PMID:8996088
A;Residues: 1-320 <TRI>A;Molecule type: Drotein
A;Rocession: PC4414
A;Molecule type: protein
A;Molecule type: Drotein
A;Genetics:
A;Genetics

Query Match

41.3%; Score 52; DB 2; Length 320;

```
A,Gene: Ac-lers
C,Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                    252 RGDADINTFAGDSASWK 268
                                                                                                                                                                                                                                                                                                                                                               6 RGDNDISPFSGDGQPFK 22
                                                                                                                A,Gene: BME10562
A,Map position: I
C,Keywords: glycosidase; hydrolase
                     A;Cross-references: GB:AE008917; F
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNKIQEYYGDSÓSFKD 76
                                                                                                                                                                                                                                    Match 38.1%;
Local Similarity 52.9%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 DNDISPFSGDGQPFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <LIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-385 <AYR>
   · KGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-385 <KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T41811
A:Residues: 1-277
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T41811
                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                             neural cell adhesion molecule L1 - rat

N'Alternate names: nerve growth factor-inducible large external glycoprotein; NILE glyco
S'Species: Rattures norvegicus (Norway rat)
C'Species: Rattures norvegicus (Norway rat)
C'Species: 13-40n-1995 #sequence revision 13-7an-1995 #text_change 20-Aug-1999
C'Accession: S36126; S17655; Ā60917; A30326
R'Miura, M.; Kobayashi, M.; Asou, H.; Uyemura, K.
FEBS Lett. 289, 91-95, 1991
A'Title: Molecular cloning of cDNA encoding the rat neural cell adhesion molecule L1. Tw
A'Reference number: S17655; MUID:91372414; PMID:1894011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: Characterization of a partial cDNA clone for the NILE glycoprotein and identifi A,Reference number: A60917; MUID:89257627; PMID:2723751 A,Accession: A60917 A,Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1159-1199, 'G', 1201-1235, 'K', 1237 <PRI>
A; Neusidues: 1159-1199, 'G', 1201-1235, 'K', 1237 <PRI>
A; Note: this paper appeared earlier, with printing errors, as reference A30326
B; Prince, J.T.; Milona, N.; Stallcup, W.B.
J. Neurosci. 9, 876-883, 1989
A; Neurosci. 9, 876-883, 1989
A; Title: Characterization of a partial cDNA clone for the NILE glycoprotein and identifitherence number: A30326; MUID:89177485; PMID:2466866
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Note: this paper was reprinted as reference A60917 to correct the omission of several C; Comment: This sequence of this surface-accessible glycoprotein differs at only two post accessible only after treatment of cells with detergent and is assumed to be cytoplasmi C; Superfamily: neural cell adhesion molecule Li, fibronectin type III repeat homology; i C; Keywords: cell adhesion; duplication; glycoprotein; membrane protein F;531-592/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: AD3322
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lysozyme (EC 3.2.1.17) - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-1178,1183-1259 <MI2>
A;Cross-references: EMBL:X59149; NID:g56740; PIDN:CAA41860.1; PID:g56741
A;Prince, J.T.; Milona, N.; Stallcup, W.B.
J. Neurosci. 9, 1825-1834, 1989
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1259;
                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
58.8%; Pred. No. 3.3; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.3%; Score 49.5; 1
66.7%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLÓERGDSD-KYFIEDGO 574
                                                                                                                                         112 TDLDDRGGNDIPYLTGD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DLQERGDNDISPFSGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1259 «MIU»
A;Cross-references: EMBL;X59149
A;Accession: S17655
                                                                                          1 TDLQERGDNDISPFSGD
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: AD3322
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S36126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
```

```
A;Cross-references: GBL22858; NID:g510708; PIDN:AAA66697.1; PID:g559136
R;Li, Y.; Passarelli, A.L.; Miller, L.K.
J. Virol. 67, 5260-5268, 1993
A;Title: Identification, sequence, and transcriptional mapping of lef-3, a baculovirus ge A;Reference number: A40677; MuID:93353600; PMID:8350397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: D72858; A40677 — Tevision 12-Nov-1999 #text_change 24-Nov-1999 R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. A;Iriology 202, 586-605, 1994 A;Atitle: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus. A;Reference number: A72850; MUID:94303173; PMID:8030224
                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
PIDN: AAL51743.1; PID: 917982481; GSPDB: GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T41811
R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: Z22020; MUID:99281911; PMID:10355780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             late expression factor 3 - Autographa californica nuclear polyhedrosis virus
C.Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A.Note: dsDNA virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63740.1; PID:g3745893
A;Experimental source: isolate T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEF-3 orf67 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A;Variety: isolate T3
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:L18873; NID:g349019; PIDN:AAA02964.1; PID:g349020
A,Note: authors translated the codon ACA for residue 92 as Tyr
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                  Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 385;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
17;
                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                  DB :
                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                  Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.1%; Score 48; 56.2%; Pred. No.
```

```
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayaahi, I.; Cui, L.; Oguch ma, A.; Mizutani-Ui, Y.; Kobayaahi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatau, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MuID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cjaccession: I61186
Riziober, B.L.; Vu, M.P.; Waleh, N.; Crawford, J.; Lin, C.S.; Kramer, R.H.
J. Biol. Chem. 268, 26773-26783, 1993
A;Title: Alternative extracellular and cytoplasmic domains of the integrin alpha 7 subuns
A;Reference number: A49691; MUID:94075378; PMID:8253814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-825 «KUR»
A;Cross-references: GB:BA000018; PID:g13701417; PIDN:BAB42711.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1447
     C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B89944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     integrin alpha chain - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1994 #sequence_revision 14-Jul-1995 #text_change 29-Sep-1999
C;Accession: S38783; S23600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Species: Mus musculus (house mouse)
C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A/Status: preliminary
A/Molecule type: mRNA
A/Rosiduse: 1-116,'118-349,'D',351-804,'R',806,'V',808-1106 <SON>
A/Cross-references: EMBL:X65036
C/Superfamily: integrin alpha-2b chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46.5; DB 2;
Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 2;
Pred. No. 55;
0; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
36.9%; Score 46.5; D
Best Local Similarity 47.8%; Pred. No. 91;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Kaufman, S.J.
submitted to the EMBL Data Library, March 1992
A.Reference number: 838783
A.Accession: 838783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 DĽNQDĠFPĎÍAVGAPPOGĎĠKVP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DLQERGDNDI --- SPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 GDEDOLPSVGPGOVFKD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.3%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 GDNDISPFSGDGQPFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.8°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-7 integrin - mouse
                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                       intracellular alkaline serine proteinase aprX [imported] - Bacillus halodurans (strain C Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Do-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: B83891
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83891
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-444 <STO>
A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05649.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: aprX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Global stress requirement protein GarA (imported) - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: O2.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C;Accession: A40400
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: AH0410
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB: AL590842; PIDN: CAC92612.1; PID: g15981308; GSPDB: GN00175
C; Genetics:
A; Gene: gsrA
C; Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SA1447 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.3%; Score 47; DB 2; Length 444; Best Local Similarity 47.1%; Pred. No. 28; Matches 8; Conservative 4; Mismatches 5; Indels
                                                                              Query Match 38.1%; Score 48; DB 2; Length 385; Best Local Similarity 56.2%; Pred. No. 17; Matches 9; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2
Pred. No. 30;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :| |:|::||| |
DTTDREDDDVAPFSSRG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DLQERGDNDISPFSGDG 18
                                                                                                                                                                                       8 DNDISPFSGDGOPFKD 23
                                                                                                                                                                                                                            61 DNKIQEYYGDSQSFKD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GDNDISPFSGDGOPFK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 GDN--SPFCQDGSPFQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.5%;
Matches 10; Conservative
C;Genetics:
A;Note: lef-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
B89944
                                                                                                                                                                                                                                       a
                                                                                                                                                                                          ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

us-09-812-485a-49.rpr

```
nuclectidyltransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD3154
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
A;Athuthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pypothetical protein AGR_L_62 [imported] - Agrobacterium tumefaciens (strain CS8, Cereon)|
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: E98133
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A;title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-adenosylmethionine-tRNA ribosyltransferase-isomerase (EC 5.4.99.-) queA PA3824 [similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
                                                                                                                                                                                                                                                                                                                                                                      Ititle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.; Hickey,
A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-308 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45650.1; PID:g17743374; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE007870; PIDN:AAK88591.1; PID:g15158304; GSPDB:GN00170
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83170
R;Stcover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ore 46; DB 2; Length 365;
ed. No. 32;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 GAREISNFLNDGOPF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 GAREISNFLNDGOPF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 GDNDISPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GDNDISPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: E98133
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <KUR>
                                                                                                                                                                                                                                                                                                                                               ster, E.W.
A; Title: The Genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: AD3154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: Atu4856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: AGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: JC5951
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-657,733-1137 <LEU2>
A;Cross-references: GB:AF032108
R;Wang, W:; Wu, W.; Desai, T.; Ward, D.C.; Kaufman, S.J.
Genomics 26, 535-570, 1995
A;Title: Localization of the alpha7 integrin gene (ITGA7) on human chromosome 12q13: clu
A;Reference number: A56839
A;Accession: A56839
A;Accession: A56839
A;Actus: preliminary
A;Molecule type: mRNA
A;Residues: 664-666,668-688,690-825,'X',827-839,'D',841-946,'H',948,'T',951,'P',953-1052
A;Cross-references: EMBL:X7425; NID:9437781
R;Gong, W.K.: Wang, W.; Sato, H.; Bielser, D.; Kaufman, S.
submitted to the EMBL Data Library, July 1993
A;Description: Expression of alpha 7 integrin cytoplasmic domains during skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Sep-1998 #sequence revision 04-Sep-1998 #text_change 31-Dec-2000
C;Accession: UC5950; UC5951; Ā56839; 840147
R;Leung, E.; Lim, S.P.; Berg, R.; Yang, Y.; Ni, J.; Wang, S.; Krissansen, G.W.
Biochem. Biophys. Res. Commun. 243, 317-325, 1998
A;Title: A novel extracellular domain variant of the human integrin alpha 7 subunit gene A;Reference number: UC5950; MUID:98139911; PMID:9473524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Map position: 12q13-12q13
C; Superfamily: integrin alpha-2b chain
C; Keywords: glycoprotein; skeletal muscle; transmembrane protein
C; Keywords: glycoprotein; skeletal muscle; transmembrane protein
F; 1-33/Domain: signal sequence #status predicted <SIG>
F; 34-1137/Product: integrin alpha-7 chain, long splice form #status predicted <MATL>
F; 1038-1056/Domain: transmembrane #status predicted <TRM>
F; 1038-1056/Domain: transmembrane #status predicted <TRM>
F; 86, 742, 945, 981, 1001/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-1137 <LEU1>
A;Cross-references: GB:AF032108; NID:g2897115; PIDN:AAC39708.1; PID:g2897116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: S40147
A;Accession: S40147
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 1061-1137 <SON>
A;Cross-references: EMBL:X74295; NID:g437781; PIDN:CAA52348.1; PID:g437782
A;Gene: GDB.ITGA7
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                          A,Residues: 1-1135 <RES>
A,Cross-references: GB:L23423; NID:g431415; PIDN:AAA16600.1; PID:g431416
C,Superfamily: integrin alpha-2b chain
                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1137;
                                                                                                                                                       Length 1135;
                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                       2;
                                                                                                                                                       DB
                                                                                                                                                ; Score 46.5; DE; Pred. No. 94; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.9%; Score 46.5; I
47.8%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:131465; OMIM:600536
                                                                                                                                                                                                                                                                                                                                           DLNODGFPDIAVGAPFDGDGKVF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLNQDGFPDIAVGAPFDGDGKVF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JC5950
integrin alpha-7 chain precursor - human
                                                                                                                                                                                                                                                                                    2 DLQERGDNDI --- SPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DLQERGDNDI --- SPFSGDGQPF 21
                                                                                                                                                Query Match 36.9%;
Best Local Similarity 47.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 11; Conserv
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

ö

M.J.; Bri K.; Lim,

ö

```
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83170
A;Status: presimary
A;Retus: presimary
A;Residues: 1-347 <STO>
A;Residues: 1-347 <STO>
A;Cross-references: GB:AE004799; GB:AE004091; NID:g9949981; PIDN:AAG07211.1; GSPDB:GN001
A;Experimental source: strain PAO1
A;Genetics:
C;Genetics:
C;Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
36.1%; Score 45.5; DB 2; Length 347;
Best Local Similarity 42.9%; Pred. No. 36;
Matches 9; Conservative 3; Mismatches 2; Indels
```

Search completed: January 29, 2004, 12:40:57 Job time : 17.3421 secs

8 8

THIS PAGE BLANK (USPTO)

```
NCBI_TaxID=1061
                                                                                                                                                                                                                                                        RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAND
STRAND
TURN
                                                                                                                                                                                                                        RESULT 1
PORI_RHOCA
ID PORI_RI
                                                                                                                                                                                                                                                           mus musculu
homo sapien
pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drosophila
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chlamydia m
chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P31243 rhodobacter
Q05695 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ustilago ma
bacillus am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c ileal sod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scyliorhinu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  halobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              halobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lycopersico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human papil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autographa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                January 29, 2004, 12:35:18 ; Search time 12.7105 Seconds (without alignments) 85.096 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q63258 1
Q61738 1
Q13683 H
Q9bxh8 E
Q9v7a4 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8vig3
Q8wyr4
Q8wyr4
P54424
P51130
P50821
Q10366
P32689
P32689
Q60414
Q60414
Q60414
Q60917
Q95934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P11688
044386
P81130
P33452
Q15911
P00742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09w1m8
051968
048313
042463
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                          127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                        126
1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PORI_RHOCA
CAML_RAT
LEF3_NPVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUEA_PSEAE
TIA4_DRONE
CAML_MOUSE
TSA2_MOUSE
TSA2_HUNAN
GUNI_USTMA
SACB_BACM
SACB_BACM
VL1 HPV60
YDBG_SCHPO
YDBG_SCHPO
YDBG_SCHPO
TTA5_XENLA
ITA5_XENLA
ITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RL2_CHLMU
COBT_PEEDE
ITAS_MOUSE
ITAS_MOUSE
ITAS_DOONE
COCC_SCYCA
RPSD_AGRYS
ABF1_HUWAN
ABF1_HUWAN
ITAS_DROWE
GVO1 HLM1NI
GVO1 HALNI
DCL_IYCES
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        - protein search, using sw model
                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
                                                                                                                                    US-09-812-485A-49
126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03
                                                                                                                                                                                                                                                                                                                                                                                                     SwissProt_41:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472
508
851
698
1050
348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475
284
284
631
1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44444 44

WWWWW 64

4 . . . . . 4444 . . . 444

4 N N N N W W W W W W W C C C C
                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                      OM protein
                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                            Searched:
                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
```

P77608 escherichia										
MHPD_ECOLI	Y354_CLOPE	HRCA_RHIME	SLP2_DROME	FLIF RHIME	SYL DEIRA	AKY1 HUMAN	METH MYCTU	TRI1_ECOLI	VHED_BPT3	FAEH_ECOLI
Н.	4 ~4	-	-	-	ч	٦	٦	٦	~	-
269	294	359	445	557	823	941	1192	1756	232	265
e, c		'n	m	m	۳.	'n	m	m	0	o.
33.3	3 8	33	33	33	33	33	33	33	32	32
4.2	4 4 2 2	42	42	42	42	42	42	42	41.5	41.5
8. c	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
-!- SUBUNIT: Homotrimer.
-!- SUBCELJULAR LOCATION: Integral membrane protein. Outer membrane.
-!- DOMAIN: THE MONOMER CONSISTS OF A 16-STRANDED ANTIPARALLEL BETA-
-!- DOMAIN: THE MONOMER CONSISTS OF A 16-STRANDED ANTIPARALLEL BETA-
PLEATED SHEET BARREL (171 RESIDUES), THREE SHORT ALPHA-HELICES (18
RESIDUES) AND 13 HYDROGEN-BONDED REVERSE TURNS (26 RESIDUES).
PIR; $16000; $15.0UL-93.
PDB; 3POR; 15-JUL-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=93021091; PubMed=1328651;
Weiss M.S., Schulz G.E.;
"Structure of porin refined at 1.8-A resolution.";
"J. Mol. Biol. 227:499-509(1992).
-!- FUNCTION: FORMS CHANNELS THAT ALLOW THE PASSIVE DIFFUSION OF SMALL HYDROPHILIC SOLUTES UP TO AN EXCLUSION LIMIT OF ABOUT 0.6 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiss M.S., Wacker T., Weckesser J., Welte W., Schulz G.E.; "The three-dimensional structure of porin from Rhodobacter capsulatus
                                                                                                                                                                                                                Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DSM 938 / 37b4;
MEDLINE=9192114; PubMed=1707373;
MEJSS M.S., Kreusch A., Schiltz E., Nestel U., Welte W.,
Weckesser J., Schulz G.E.;
"The structure of porin from Rhodobacter capsulatus at 1.8-A
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=DSM 938 / 37b4;
MEDLINE=91330909; PubMed=1651239;
MEDLINE=91330909; PubMed=1651239;
MEDLINE=91330909; PubMed=1651239;
Sprintz B., Kreusch A., Mestel U., Schulz G.E.;
Fyring Structure of porin from Rhodobacter capsulatus.";
Fur. J. Biochem. 199:587-594(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane; Transmembrane; Porin; 3D-structure,
                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
   301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DSM 938 / 37b4;
MEDLINE=90336791; PubMed=2165921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resolution.";
FEBS Lett. 280:379-382(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at 3-A resolution.";
FEBS Lett. 267:268-272(1990)
STANDARD;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X59149; CAA+1.

DR HIR; S36126; S36126.

DR HIR; S36126; S36126.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR003981 Ig_c2.

DR InterPro; IPR003006; Ig_MHC.

DR Ffam; PP00041; fin3; 4.

DR Pfam; PR00041; fin3; 4.

DR Pfam; PR00046; FN3; 4.

DR PRAFT; SM00066; FN3; 4.

DR SWART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG_LIKE; 6.

RW SWART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG_LIKE; 6.

RW SWART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG_LIKE; 6.

RW SWART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG_LIKE; 6.

RW SWART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG_LIKE; 6.

RW SWART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG_LIKE; 6.

RW SWART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG_LIKE; 6.

RW SWART; PS50835; IG_LIKE; 6.

PROSITE; PS50835; IG_L
ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC. BINDS TO AXONIN ON NEURONS. SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS:
                                                                                                                                         Name=2; Synonyms=Llcs;
Isoid=005695-2; Sequence=VSP 002592;
TISSUE SPECIFICITY: THE SHORTER ISOFORM IS PREDOMINANTLY FOUND IN
THE BRAIN, WHILE THE LONGER ISOFORM IS FOUND IN THE PERIPHERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
N. LINKED (GLONAC. . ) (POTENTIAL).
N. LINKED (GLONAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                     Name=1;
IsoId=005695-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NERVOUS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SITE
         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-9137244; PubMed=1894011;
Miura M., Kobayashi M., Asou H., Uyemura K.;
Miolecular cloning of cDNA encoding the rat neural cell adhesion
molecule L1. Two L1 isoforms in the cytoplasmic region are produced
by differential splicing.";
FEBS Lett. 289:91-95(1991).
-!- FUNCTION: CELL ADHESION MOLECULE WITH AN IMPORTANT ROLE IN THE
DEVELOPMENT OF THE NERVOUS SYSTEM. INVOLVED IN NEURON-NEURON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.3%; Score 52; DB 1; Length 301; 58.8%; Pred. No. 0.99; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31536 MW; 4C57149C348D2943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FFB-1994 (Rel. 28, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEB-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule L1 precursor (N-CAM L1).
L1CAM OR CAMLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 TOLDDRGGNDIPYLTGD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TDLQERGDNDISPFSGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.8
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292
301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAND
STRAND
SEQUENCE
                                                                                   STRAND
TURN .
STRAND
STRAND
HELIX
                                                                                                                                                                                                                     STRAND
TURN
STRAND
TURN
                                                                                                                                                                                                                                                                                                                                                       STRAND
STRAND
TURN
STRAND
STRAND
STRAND
STRAND
TURN
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TURN
                                                                                                                                                                                                                                                                                                 STRAND
STRAND
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELIX
                                                                                                                                                                                 TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URN
```

8

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyhedrosis virus.";
Virology 202:886-605(1994).
-!- FUNCTION: REQUIRED FOR LATE AND VERY LATE GENE EXPRESSION. LEF-3
COULD BE A SINGLE STRANDED DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li Y., Passarelli A.L., Miller L.K.; "Identification, sequence, and transcriptional mapping of lef-3, a baculovirus gene involved in late and very late gene expression.";
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                        DB 1; Length 1259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R. The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Autographa californica nuclear polyhedrosis virus (ACMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.1%; Score 48; DB 1; Length 385; 56.2%; Pred. No. 5.6;
                                                                                                                                                                                                      0F12A7C4415F3C08 CRC64;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Early protein; Transcription regulation; DNA-binding. SEQUENCE 385 AA; 44551 MW; 9A25ECD7BA7FBDF1 CRC64;
                                                                                                                                                       (in isoform 2)
                                                                                                   (GLCNAC.
                                                    (GLCNAC.
  (GLCNAC.
                                                                                                                                  (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                        Score 49.5; DE
Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
  N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94303173; PubMed=8030224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=L1;
MEDLINE=93353600; Pubmed=8350397;
                                                                                                                                                                                                         AA; 140934 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             558 DLQERGDSD-KYFIEDGQ 574
                                                                                                                                                                                                                                                                                                                                                           2 DLOERGDNDISPESGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seqn
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virol. 67:5260-5268(1993).
                                                                                                                                                                                                                                                        39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L18873; AAA02964.1; -. EMBL; L22858; AAA6697.1; -. PIR; D72858; D72858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNDISPESGDGQPFKD 23
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7'
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Late expression factor 3
                                                    1021
1029
1072
1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=46015;
  968
978
1021
1029
1106
                                                                                                                                                                                                         1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEF3 NPVAC
P41453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C6;
  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                      CARBOHYD
                                                                                 CARBOHYD
                                                                                                      CARBOHYD
                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
LEF3 NPVAC
LEF7 NPVAC
AC P41453,
DT 01-NOV-
RR MEDLIN
RC STRAIN
RT 0-10-NO-
RT 0-1-FO
CC 0-1-FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
     SHIFFFFF
                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

DNKIQEYYGDSQSFKD 76

ద

```
MEDLINE=96197131; PubMed=8626012;

AMETINE=96197131; PubMed=8626012;

MINEDLINE=96197131; PubMed=8626012;

MINEDLINE=96197131; PubMed=8626012;

MINEDLINE=96197131; PubMed=8626012;

AND STATE IN GENERAL STATE IN GRAPH, and alpha?B integrins with the meuromuscular junction.";

AND STATE INTEGRIN ALBHA-7/BETA-1 IS THE PRIMARY LAMININ RECEPTOR ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC

ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC

ON SKELETAL MYOBLASTS AND PACILITATE THEIR LOCALIZATION AT LAMININ-RICH SITES OF SECONDARY FIBER FORMATION. INVOLVED IN THE MAINTENANCE OF SITES OF SECONDARY FIBER FORMATION. INVOLVED IN THE MAINTENANCE OF THE MYOFIBERS CYTOARCHITECTURE AS WELL AS FOR THEIR ANCHORAGE,

VIABILITY AND FUNCTIONAL INTEGRITY.

SUBBUNIT: HETERODIMER OF AN HEAVY AND A LIGHT CHAIN LINKED BY A SUBJUSTION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: ISOFORMS ARE DEVELOPMENTALLY REGULATED DURING THE FORMATION OF SKELETAL MUSCLE. ISOFORMS A AND C ARE INDUCED UPON TERMINAL MYOGENIC DIFFERENTIATION; ISOFORMS A B IS PRESENT EARLIER IN REPLICATING CELLS AND DIMINISHES UPON DIFFERENTIATION. PTM: ADP-RIBOSYLATED ON AT LEAST TWO SITES IN THE EXTRACELLULAR DOMAIN IN SKELETAL MYOTUBES (BY SIMILARITY).

SIMILARITY: CONTAINS TO THE INTEGRIN ALPHA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skeletal muscle;
MEDLINE=94171924; PubMed=8126096;
Song W.K., Wang W., Saco H., Bieleer D.A., Kaufman S.J.;
Song W.C., Wang W. Saco H., Bieleer D.A., Kaufman S.J.;
Expression of alpha 7 integrin cytoplasmic domains during skeletal
muscle development: alternate forms, conformational change, and
homologies with serine/threonine kinases and tyrosine phosphatases.";
J. Cell Sci. 106:1139-1152(1993).
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOIG-661258-3; Sequence-VSP 002735; TISSUE SPECIFICITY: EXPRESSED IN SKELETAL AND CARDIAC MUSCLE. EXPRESSED IN REPLICATING MYOBLASTS. IN DIFFERENTIATED MUSCLE FIBERS LOCALIZES BETWEEN FIBERS AND THE SURROUNDING MATRIX. ISOFORMS A AND B ARE EXPRESSED AT MYOTENDINOUS AND NEUROMUSCULAR JUNCTIONS; ISOFORM C IS EXPRESSED AT NEUROMUSCULAR JUNCTIONS AND
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM ALPHA-7XIB).
TISSUE=Skeletal muscle;
MEDLINE=92242309; PubMed=1315319;
Song W.K., Wang W., Foster R.F., Bielser D.A., Kaufman S.J.;
H316-alpha 7 is a novel integrin alpha chain that is developmentally regulated during skeletal myogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS ALPHA-7X1A AND ALPHA-7X1C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
Q63258; Q63026; Q63327; 1106 AA. 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 18-EB-2003 (Rel. 41, Last annotation update) Integrin alpha-7 (H36-alpha7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Alpha-7X1A;
IsoId=Q63258-2; Sequence=VSP_002734;
Name=Alpha-7X1C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId-Q63258-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AT EXTRASYNAPTIC SITES
                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Alpha-7X1B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY.
```

362 DLNQDGFPDIAVGAPFDGDGKVF 384

엄

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                  EMBL; X65036; CAA46170.1; -.

REMBL; X74293; CAA52347.1; -.

REMBL; X74293; CAA52347.1; -.

REMBL; X74294; CAA52347.1; -.

REDIT, X74294; CAA52347.1; -.

REDIT, X74294; CAA52347.1; -.

REDIT, X74294; CAA52347.1; -.

REDIT, X38783; S38783.

REPETATO, IPROGA13; Integrin_A; I.

REPTATO, REPUTATOR INTEGRINA.

REPTATOR INTEGRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
LGFFKRAKHPEATVPQYHAVKILREDRQGFKEEKTGTIQRS
NWGNSGDSAPHPILAADMHELGABGHPVKATA. -> CG
FFRRNSPSSSFPANYHRAHAAVQSAMEAGGFGTVGWDSSS
GRSTLRPLYPSTTQ (in isoform Alpha-7XlA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAKHPEATVPQYHAVKILREDRQQFKEEKTGTIQRSNWGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QWEGSDAHPILAADWHPELGPDGHPVSVTA ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILA.
BY SIMILARIT.
BY SIMILARIT.
BY SIMILARITY.
BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILSIY (in isoform Alpha-7X1C) /Frid=VSP_002735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFFKR MOTIF.
3 X 4 AA REPEATS OF D-X-H-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW; 21B2A187837E01F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTIG=VSP 002734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46.5; I
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FG-GAP 1.
FG-GAP 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1106 AA; 121101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%;
ilarity 47.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1003
1029
1106
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1036
1101
1085
1093
1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1082
1090
1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DOMAIN
TRANSMEM
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
REPEAT
CA BIND
CA BIND
CA BIND
CA BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
```

```
MEDLINE=96197133; PubMed=8626012;
Martin P.T., Kaufman S.J., Kramer R.H., Sanes J.R.;
"Synaptic integrins in developing, adult, and mutant muscle: selective
association of alpha1, alpha7A, and alpha7B integrins with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kramer R.H., Vu M.P., Cheng Y.F., Ramos D.M., Timpl R., Waleh N.; "Laminin-binding integrin alpha 7 beta 1: functional characterization and expression in normal and malignant melanocytes."; Cell Regul. 2:805-817(1991).
                                                                                                                                                                                                                 SECUENCE FROM N.A. (ISOPORMS ALPHA-7A; ALPHA-7X2B AND ALPHA-7X1X2). SECUENCE FROM N.A. (ISOPORMS ALPHA-7A; ALPHA-7X2B AND ALPHA-7X1X2). STRAIN=BALB/c; TISSUE=Heart; MEDLINE=94075378; PubMed=8253814; Ziober B.L., Vu M.P., Waleh N., Crawford J., Lin C.-S., Kramer R.H. "Alternative extracellular and cytoplasmic domains of the integrin alpha 7 subunit are differentially expressed during development."; J. Biol. Chem. 268:26773-26783(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ziober B.L., Kramer R.H.; Indentification of the cell type-specific and developmentally regulated alpha7 integrin gene promoter."; J. Biol. Chem. 271:22915-22922(1996).
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93366824; PubMed=8360188;
Collo G., Starr L., Quaranta V.;
A new isoform of the laminin receptor integrin alpha 7 beta 1:
developmentally regulated in skeletal muscle.";
J. Biol. Chem. 268:19019-19024(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mayer U., Saher G., Fassler R., Bornemann A., Echtermeyer F., von der Mark H., Miosge N., Poeschl E., von der Mark K.; "Absence of integrin alpha 7 causes a novel form of muscular
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS ALPHA-7X1X2A AND ALPHA-7X1X2B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE FROM N.A. (ISOFORMS ALPHA-7A AND ALPHA-7B)
STRAIN=C57BL/6 X BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                   Saher G., Echtermeyer F., Beier D.R., Poeschl E., Mayer U. "Genomic organization and chromosomal localization of the integrin alpha? gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrin alpha7 gene.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
TTA7_MOUSE STANDARD; PRT; 1179 AA. Q61738; 088731; 088732; P70350; Q61737; Q61741; 116-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 34-58.
TISSUE=Melanoma;
MEDLINE=92198982; PubMed=1839357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98016417; PubMed=9354797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96394366; PubMed=8798472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuromuscular junction.";
Dev. Biol. 174:125-139(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 17:318-323(1997)
                                                                                                 Integrin alpha-7 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-70 FROM N.A. STRAIN=C57BL/6 X CBA;
                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY.
                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP-RIBOSYLATION
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dystrophy.
```

۲;

Gaps

3,

Indels

. 9

3; Mismatches

11;

Matches

DLQERGDNDI --- SPFSGDGQPF 21

---

```
INTEGRIN ALPHA-7 HEAVY CHAIN (POTENTIAL)
INTEGRIN ALPHA-7 LIGHT CHAIN (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Premission Procession Annuagran alpha.

Premission Procession Annuagran A. 1.

Procession Annuagran Annuagran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFFKR MOTIF.
3 X 4 AA REPEATS OF D-X-H-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL). FG-GAP 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46.5; DB 1;
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITA7 HUMAN
ID TITA7 HUMAN STANDARD; PRT; 1181 AA.
AC Q13683; 043197; Q9NY89; Q9UETO; Q9UEV2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FG-GAP 7.
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FG-GAP 2.
FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 DLNQDGFPDIAVGAPFDGDGKVF 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L16544; -; NOT ANNOTATED_CDS.
PIR; 161186; 161186.
HSSP, P11215; 1A8X.
MGD; MGI.102700; Itga7.
InterPro; IPR000413; Integrin_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DLQERGDNDI --- SPFSGDGQPF 21
                         JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                         JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
                                                                                                                                                                                                                                                                          JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          955
11179
11076
11002
11179
1179
1174
124
124
1400
459
459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L23421; AAA16598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
959
34
1077
1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y12382;
                                                                             (12388;
                                                                                                     (12389;
                                                                                                                              Y12390;
                                                                                                                                                                                                       112380;
                                                                                                                                                                                                                                                                                                                                                                                                       Y12390;
                                                        712387
                                                                                                                                                                                                                                                                                                                                                                                                                                 Y12381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA_BIND
CA_BIND
CA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
  EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
     "IBOID # OF TAKEAT' ISOPORMS CONTAINING SEGMENT X2 ARE FOUND IN ADMINISTRATE TO THE STORMS CONTAINING SEGMENT X2 ARE FOUND IN ADULT HEART, LUNG AND IN PROLIFERATING SKELETAL WYOBLASTS BUT NOT IN ADULT SKELETAL WUSCLE. ISOFORMS CONTAINING SEGMENT X1 ARE EXPRESSED IN ADULT IN ADULT SKELETAL WUSCLE. ISOFORMS CONTAINING SEGMENT A ARE EXCIDENTED TO SKELETAL WUSCLE. ISOFORMS CONTAINING SEGMENT B ARE WIDELY EXPRESSED IN WUSCLE ISOFORMS CONTAINING SEGMENT A AND B ARE EXPRESSED AT WYOTENDINOUS AND NEUROWUSCULAR JUNCTIONS, ISOFORMS CONTAINING SEGMENT A NEUROWUSCULAR JUNCTIONS AND AT EXTRASYNAPTIC SITES.

- DEVELOPMENTAL STAGE: ISOFORMS ARE DEVELOPMENTALLY REGULATED DURING FORMATION OF SKELETAL MUSCLE. UNDIFFERENTIATED (REPLICATING) MYOBLASTS EXPRESS ISOFORMS CONTAINING SEGMENT B ONLY, WHEREAS DIFFERENTIATED MYOBLASTS EXPRESS ISOFORMS CONTAINING SEGMENT B ONLY, WHEREAS
                                                                     THE MYOLIBER AND FACTORISE AND ADULT MYOLIBERS. DURING MYOGENIC ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC OF MYOBLASTS, AND FACILITATE THEIR LOCALIZATION AT LAMININ-RICH SITES OF SECONDARY FIBER FORMATION. INVOLVED IN THE MAINTENANCE OF THE MYOFIBERS CYTOARCHTECTURE AS WELL AS FOR THEIR ANCHORAGE, VIABILITY AND FUNCTIONAL INTEGRITY. MICE CARRYING A ITGAT NULL ALLELE ARE VIABLE AND FERTILE, BUT SHOW PROGRESSIVE MUSCULAR DYSTROBILITY IN DIFFERENT MUSCLE TYPES.

'VARIABILITY IN DIFFERENT MUSCLE TYPES.

'SUBUNIT: HETERODIMER OF AN HENYY AND A BETA SUBUNIT. THE ALPHA SUBUNIT IS COMPOSED OF AN HENYY AND A LIGHT CHAIN LINKED BY A DISLULDIDE BOUND ALPHA A ASSOCIATES WITH BETA-1.

'SUBCELLULAR LOCATION: TYPE I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event—Alternative splicing; Named isoforms=6;

Comment-Additional isoforms seem to exist. There is a combination of at least four alternatively spliced domains, two extracellular (X1 and X2) and two cytoplasmic (A and B). A third potential alternatively spliced cytoplasmic (A and B). A third appear to be expressed. So far detected are isoforms alpha-7XIA, alpha-7XIB and alpha-7XIB. Experimental confirmation may be lacking for some isoforms;

Name=Alpha-7XIX2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- PTM: ADP-RIBOSYLATED ON AT LEAST TWO SITES OF THE EXTRACELLULAR DOMAIN IN SKELETAL MYOTUBES (IN VITRO).

-i- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

-i- SIMILARITY: CONTAINS 7 PG-GAP PEPEATE.
MEDLINE-95238432; PubMed=7721841;
Zolkiewska A., Moss J.;
"Processing of ADP-ribosylated integrin alpha 7 in skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-Alpha-7x1A;
IsoId=Q61738-2; Sequence=VSP_002732, VSP_002733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Alpha-7X2A;
IsoId=Q61738-4; Sequence=VSP_002731, VSP_002733;
Name=Alpha-7X2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1sold=Q61738-5; Sequence=VSP_002731;
Name=Alpha-7X1X2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q61738-3; Sequence=VSP_002732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=061738-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U60419; AAC5272.1; -.
Y12380; CAA73023.1; -.
Y12383; CAA73023.1; JOINED.
Y12384; CAA73023.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L23423; AAA16600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Alpha-7X1B;
```

á

Gaps

3,

Indele

EMBL; EMBL; EMBL; EMBL;

Length 1179;

```
FUNCTION.
                                                                                                                                                                 FUNCTION
                                                                                                                           domain."
  MEDLINE=92198982; PubMed=1839357; Kramos D.M., Timpl R., Waleh N.; Kramer R.H., Vu M.P., Cheng Y.F., Ramos D.M., Timpl R., Waleh N.; "Leminin-binding integrin alpha 7 beta 1: functional characterization and expression in normal and malignant melanocytes."; Cell Regul. 2:805-817(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Song W.K., Wang W., Sato H., Bielser D.A., Kaufman S.J.; "Expression of alpha 7 integrin cytoplasmic domains during skeletal muscle development: alternate forms, conformational change, and homologies with serine/threonine kinases and tyrosine phosphatases."; J. Cell Sci. 106:1139-1152(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Heart;
MEDLINE=94075378; PubMed=8253814;
Ziober B.L., Vu M.P., Waleh N., Crawford J., Lin C.-S., Kramer R.H.;
"Alternative extracellular and cytoplasmic domains of the integrin alpha 7 subunit are differentially expressed during development.";
J. Biol. Chem. 268:26773-26783(1993).
                                                                                                                                                                                                      "A novel extracellular domain variant of the human integrin alpha 7
                                                                                                                                                                                                                                                                         MEDLINE=98250181; PubMed=9590299;
Hayashi Y.K., Chou F.-L., Engvall E., Ogawa M., Matsuda C.,
Hirabayashi S., Yokochi K., Ziober B.L., Kramer R.H., Kaufman S.J.,
Ozawa E., Goto Y.-I., Nonaka I., Tsukahara T., Wang J.Z.,
Hoffman E.P., Arahata K.,
"Mutations in the integrin alpha? gene cause congenital myopathy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure, genetic localization, and identification of the cardion and skeletal muscle transcripts of the human integrin alpha7 gene
                                                                                   Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99333684; PubMed=10403775;
Vignier N., Moghadagzadeh B., Gary F., Beckmann J., Mayer U.,
Guicheney P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUDE-Skeletal muscle;
MEDLINE-98012902; PubMed=9352853;
Basora N., Vachon P.H., Herring-Gillam F.E., Perreault N.,
Beaulieu J.-F.;
                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS ALPHA-7X2B AND ALPHA-7X2DB)
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                TISSUE=Fetal heart, and Osteoblast;
MEDLINE=98139911; PubMed=9473524;
Leung E., Lim S.P., Berg R., Yang Y., Ni J., Wang S.-X.
Krissansen G.W.;
                                                                                                                                                                                                                     subunit generated by alternative intron splicing."; Biochem. Biophys. Res. Commun. 243:317-325(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1105-1181 FROM N.A. (ISOFORM ALPHA-7B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 260:357-364(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2).
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE FROM N.A. (ISOFORM ALPHA-7A)
                                                                                                                                                                                                                                                                                                                                                                                           Vizirianakis I.S., Ziober B.L., Kramer R.H., "Cloning of human integrin alpha-7 cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2B).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Fetal muscle;
MEDLINE=94171924; PubMed=8126096;
                                                                                                                                                                                                                                                                                                                                                          Nat. Genet. 19:94-97(1998).
                                          Integrin alpha-7 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Skeletal muscle;
                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 34-45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ".(ITGA7)."
```

```
MEDLINE=96197133; PubMed=8626012;

MEDLINE=96197133; PubMed=8626012;

MEDLINE=96197133; PubMed=8626012;

MEDLINE=96197133; PubMed=8626012;

MEDLINE=96197133; PubMed=8626012;

MEDLINE=96197133; PubMed=8626012;

MEDLINE=17, Kaumer R. H., Sanes J.R.;

MEDLINE=17, Kaumer R. H., Sanes J.R.;

MEDLINE

MEDLINE=17, Kaumer R. H., Sanes J.R.;

MEDLINE

Relation between integrin alpha7Bbetal expression in human intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event-Alternative splicing, Named isoforms=12,
Comment-Additional isoforms seem to exist. There is a
Comment-Additional isoforms seem to exist. There is a
combination of at least five alternatively spliced domains,
three extracellular (X1, X2 and D) and two cytoplasmic (A and
B). A third potential alternatively spliced cytoplasmic domain
(C) does not appear to be expressed. In vitro generated isoform
X2C shows function. So far detected are isoforms Alpha-7X1B,
Alpha-7X2B (major), Alpha-7X2DB (minor) and minor isoforms
containing segment X1X2. Experimental confirmation may be
                                                                                                                                                                                                                                                                  MEDLINE=97453229; PubMed=9307969;
Ziober B.L., Chen Y.O., Kramer R.H.;
"The laminin-binding activity of the alpha 7 integrin receptor is
defined by developmentally regulated splicing in the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q13683-4; Sequence=VSP_002728, VSP_002729, VSP_002730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q13683-8; Sequence=VSP_002727, VSP_002729, VSP_002730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schoeber S., Mielenz D., Echtermeyer F., Hapke S., Poeschl E., von der Mark K.;
"The role of extracellular and cytoplasmic splice domains of appa7-integrin in cell adhesion and migration on laminins.";
Exp. Cell Res. 255:303-313(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=013683-11; Sequence=VSP_002729, VSP_002730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q13683-2; Sequence=VSP_002728, VSP_002730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSP_002729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSP_002730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Alpha-7X2DB;
IsoId=Q13683-9; Sequence=VSP_002727, VSP_002729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q13683-6; Sequence=VSP_002727,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Alpha-7X1X2A;
IsoId=Q13683-10; Sequence=VSP_002730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q13683-5; Sequence=VSP_002728,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q13683-7; Sequence=VSP_002727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=013683-3; Sequence=VSP_002728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q13683-1; Sequence=Displayed;
                                                  cells and enterocytic differentiation."; Gastroenterology 113:1510-1521(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20160722; PubMed=10694445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Cell 8:1723-1734(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lacking for some isoforms;
Name=Alpha-7X1X2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Alpha-7X1X2DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Alpha-7X1DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Alpha-7X2DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Alpha-7X1DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Alpha-7X1B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Alpha-7X2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Alpha-7X1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Alpha-7X2A;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                             STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tohentino E., Westbrock Wadman S., Yuan Y., Bridy L.L., Coulter S.N., Folger K., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";
Nature 406:959-964(2000)."
                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Synthesizes of from preQ1 in a single S-adenosylmethionine-requiring step. The ribosyl moiety of AdoMet transferred and isomerized to the epoxycyclopentane residue of c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00113; -; 1.
InterPro; IPR003699; Queuosine_synth.
InterPro; IPR003699; Queuosine_synth.
ITGRPAMB; TIGR00113; Queuo; 1.
Queuosine_biosynthesis; Transferase; Isomerase; Complete_proteome.
SEQUENCE_347 AA; 38160 MW; 48ECBF074C2EC589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Integrin alpha-PS4 precursor (Position-specific antigen 4, alpha
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

36.1%; Score 45.5; DB 1; Length 347;
Best Local Similarity 42.9%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Queuosine biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE QUEA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1015 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 DGELKPFSGDTDIFIYPGRPF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 DNDISPFSGD-----GQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004799; AAG07211.1; -.
                        Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA-PS4 OR CG16827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
                                            NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
ITA4_DROME
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstands. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@leb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                              PIM: ADDITION OF THE STATE ON THE EXTRACELLULAR DOMAIN IN SKELETAL MYOTUBES (BY SIMILARITY).
DISEASE: DEFECTS IN ITGAT ARE ASSOCIATED WITH A FORM OF CONGENITAL MYOPATHY; A GROUP OF HETROGENEOUS MUSCLE DISORDERS WHICH ARE THOUGHT TO RESULT FROM ABNORMAL MUSCLE DEVELOPMENT. MUSCLE WEAKNESS IS EITHER NON-PROGRESSIVE OR SLOWLY PROGRESSIVE AND APPARENT FROM BIRTH OR EALLY INFANCY.
SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
SIMILARITY: CONTAINS 7 FG-GAP FEPERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5....-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.9%; Score 46.5; DB 1; Length 1181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 35;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Queuosine biosynthesis protein queA).
QUEA OR PA3824.
Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 DLNODGFPDIAVGAPFDGDGKVF 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DLQERGDNDI --- SPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAB41534.1; JOINED.
CAB41534.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF032108, AAC39708.1, EMBL, AF052050, AAC18968.1, EMBL, AF072132, AAC80458.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAB41534.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAB41534.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAB41534.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAB41534.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ228840; CAB41534.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAB41534.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAB41534.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAB41534.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAB41534.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ228849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AJ228839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ228843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ228847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUEA PSEAE
Q9HXH8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

-

EMBL;

EMBL; EMBL: EMBL;

Matches

EMBL; EMBL: RESULT 7 QUEA\_PSEAE

요 ઠ

OSCIPLIA

ï

Gape

7;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
         Rangon K.L., Rogers Y. H.C., Blazel K.C., Changle M., Pitthiler B.D.D., RA Man K.H., Doyle C., Baxter E.J., Andrews-Feankoch C., Baldwin D., Ra Ballew R.M., Basen A., An H.-J., Andrews-Feankoch C., Baldwin D., Ra Ballew R.M., Basen A., Busch E.D., Baytaktaroglu L., Beasley E.M., Beeson K.Y., Bennos P.V., Berman B.P., Bhandari D., Beasley E.M., Resorkova D., Botchan M.R., Bouck J., Baytaktaroglu L., Beasley E.M., Ra Burtis K.C., Busam D.A., Buller H., Cadiou E., Center A., Chandra I., Andrews J. Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Roden K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borsbios B., Delcher A., Gornell J.H., Gu Z., Guan P., Harris M., Cladsser K., Gorrell J.H., Gu Z., Guan P., Harris M., Alush F., Karpen G.H., Karpen G.H., Necherson D., Houston K.A., Howland T.J., Well M., Inbeyam C.J., Kraft C., Karvitz S., Kulp D., Lai Z., Linn Y., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Mourt S.M., Moy M., Murphy B., Murphy L., Muzskern D.M., Nelson K.A., Nilshina N.V., Mobarry C., Morris J., Man B., Shen H., Raington K.A., Nilshon K.A., Nilskern D.R., Porler F., Shen H., Raington K., Simpson M., Skupski M.P., Smith H., Shen K., Shen S., Follar C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith H., Sheng X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Sheng X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Sheng X., Abeng X.H., Rah, Zhong F.N., Zhong W., Zhung X., Zhung X., Zhung X., Zhong X., Zhang X., Zhung X., Zhung X., Zhong X., Zhang X., Zhung X., Zhung X., Zhung X., Zhung X., Zhong X., Zhang X., Zhung X., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: POSSIBLE ROLE IN CELL-CELL INTERACTIONS (BY SIMILARIN SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-PS4 ASSOCIATES WITH BETA-PS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FG-GAP 2.
FG-GAP 3.
FG-GAP 4.
FG-GAP 6.
FG-GAP 6.
FG-GAP 7.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01185; INTEGRINA.
SMART; SM00191; Int alpha; 4.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTEGRIN ALPHA-PS4.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FG-GAP 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003811; AAFS8154.1; -.
HSSP; P11215; 1A8X.
FlyBase; F980034005; alpha-PS4.
InterPro; IPR000413; Integrin_alpha.
Pfam; PF01839; FG-GAP; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332
394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
```

```
TISSUE-Brain;

MEDLINE-BRAIN;

MEDLINE-BRAIN;

MOOS M., Tacke R., Scherer H., Teplow D., Frueh K., Schachner M.;

MOOS M., Tacke R., Scherer H., Teplow D., Frueh K., Schachner M.;

MOOS M., Tacke R., Scherer H., Teplow D., Frueh K., Schachner M.;

Insural adhesion molecule L1 as a member of the immunoglobulin superfamily with binding domains similar to fibronectin.";

Insure 314:701-703(1988).

INALUE 314:701-703(1988).

INDEVELORMENT OF THE MERVOUS SYSTEM: INVOLVED IN NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC. BINDS

TO AXONIN ON NEURONS.

IOUS SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERPAMILY.

II SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                               1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LICAM OR CAMLI.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                            (POTENTIAL)
                            (POTENTIAL) (POTENTIAL)
                                                                                                                                  .) (POTENTIAL) .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             ъ,
                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                       DB 1; Length 1015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSS0835; IG_LIKE; 6.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
Immunoglobulin domain; Signal.
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                    MW; 964DBE424FB1FEC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule Li precursor (N-CAM Li).
                                                                                                                                  (GLCNAC.
  (GLCNAC
                                                                               (GLCNAC
                                                                                                           (GLCNAC
                                                                                                                                                                                          (GLCNAC
                                                                                                                                                                                                                                                                       Score 45.5; DB
Pred. No. 42;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                      N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                     343 DINKDGYNDVAVGAPFAGNGSVF 365
                                                                                                                                                                                                                                                                                                                                                                                  2 DLQERGDNDI --- SPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD, MGI:96721, Llcam.
InterPro; IPR003961, PN III.
InterPro; IPR00710; Ig-like.
InterPro; IPR003598; Ig-2.
InterPro; IPR003606; Ig-MHC.
Pfam; PF00041; fn3, 4.
                                                                                                                                                                                                                                                                       similarity 39.1%; Similarity 39.1%; 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X12875; CAA31368.1; -.
                                                                                                                                                                                                                       112761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00060; FN3; 2.
SMART; SM00408; IGc2; 5
455
589
607
746
821
842
853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S05479; S05479.
                                                                                                                                                                                                                       1015 AA;
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P20241; 1CFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAML_MOUSE
ID CAML_MOUSE
AC P11627;
                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
                               CARBOHYD
                                                                               CARBOHYD
                                                                                                                                                                                                                       SEQUENCE
                                                     CARBOHYD
                                                                                                           CARBOHYD
                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
A PART REPORT OF THE PROPERTY OF THE PROPERTY
```

φ,

```
ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSA2_MOUSE STANDARD; PRT; 301 AA.
Q8VIG3: Q9DALS;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Testis-specific gene A2 (Male meiotic metaphase chromosome-associated acidic protein) (Meichroacidin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthezia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                  EAIRACELDULAR (FOIENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
  ADHESION MOLECULE L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIŠSUE=Testis;
MEDLINE=98346622; PubMed=9578619;
TSuchida J., Nishina Y., Wakabayashi N., Nozaki M., Sakai Y.,
Nishimune Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22BE57001CB2A538 CRC64;
                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45.5; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     558 DLQERGDSD-KYFIEDGK 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLQERGDNDISPFSGDGQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.1%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA; 140968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1022
1030
1073
1107
20
11120
111320
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11386
11
CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1582 MOUSE
10 T9842 M
10 T9842 M
10 28-FEB
10 128-FEB
10 T 28-FEB
11 T 28-FEB

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
Rayakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Rayatawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Rayato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
Rayato K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
Ray Kuchl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackehbush J.,
Rayai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ray Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.F.,
Rayatincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Rayatincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Rayashizaki Y.,
Rasto K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Rayashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Ryunctional annotation of a full-length mouse cDNA collection.";
Rurur 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          development and its characteristic localization suggest that it may play an important role in male meiosis.
SUBCELLULAR LOCATION: Cycoplasmic in late spermatocytes, secondary spermatocytes and round spermatids. Gathered around metaphase chromosomes during meiotic divisions.
ALTERNATIVE PRODUCTS:
'Molecular cloning and characterization of meichroacidin (male meiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=Q8VIG3-2; Sequence=Not described;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Germ coll apecific. Specifically expressed in
testis, and to a lower extent in ovary. Not expressed in somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STACE: During male germ cell development it is not detected until 12 days. Significant expression is detected from 14-day-old through to adult testis. Expression is first detected in the pachytene spermatocytes at stage V, becomes stronger from the late pachytene spermatocytes to round spermatid stage, and then gradually decreases as the morphogenesis proceeds further. Not expressed in germ cells located in the first layer of the seminiferous epithelium (spermatogonia, leptotene and zygotene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 6 MORN repeats.
CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 283.
                                           metaphase chromosome-associated acidic protein).";
Dev. Biol. 197:67-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB006535; BAB83693.1; ALT_FRAME.
EMBL; AK005739; BAB24214.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=1;
IsoId=Q8VIG3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing.
POLY-GLU.
MORN 1.
                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; Pubmed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1194909; Taga2.
InterPro; IPR003409; MORN.
Pfam; PF02493; MORN; 6.
SMARY; SM00698; MORN; 6.
MGLOGIS; Repeat; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spermatocytes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
```

```
4 QERGDNDISPFSG 16
 90
113
159
309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=FBD11;
                                                                                                                                                                                                                                                                                                 USTMA
                                                         SEQUENCE
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                   GUN1 UST
P54424;
 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                        REPEAT
                                                                                                                                                                                                                                                                                GUN1_USTMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
   SFF
                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and characterization of meichroacidin (male meiotic metaphase chromosome-associated acidic protein).";
Dev. Biol. 197:67-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLUIAR LOCATION: Cytoplasmic in late spermatocytes, secondary spermatocytes and round spermatids. Gathered around metaphase chromosomes during meiotic divisions (By similarity). TISSUE SPECIFICITY: Testis specific. SIMILARITY: Contains 6 MORN repeats.
                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Testis-specific gene A2 (Male meiotic metaphase chromosome-associated
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98246622; PubMed-9578619;
Tsuchida J., Nishina Y., Wakabayashi N., Nozaki M., Sakai Y.,
Nishimune Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: May play an important role in male meiosis (By
                                                                                                                                                   35.7%; Score 45; DB 1; Length 301; 37.5%; Pred. No. 12;
                                                                                                                                                                                        4; Indels
MORN 2.
MORN 3.
MORN 4.
MORN 5.
MORN 5.
MORN 6.
P -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Testis;
Shimizu N., Kudoh J., Shibuya K.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                           309 AA
                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLU.
POLY-GLU.
MORN 1.
MORN 2.
MORN 3.
                                                                                                                                                                                                                                                                                                                                                           PRT;
 66 MO
89 MO
112 MO
135 MO
39 P
34181 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB006536; BAB83694.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB041016; BAB92995.1; -.
                                                                                                                                                                                                                            2 DLQERGDNDISPFSGD 17
                                                                                                                                                                                                                                                 :|:| |:||:
ELEEEGENDLGEYEGE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003409; MORN.
Pfam; PF02493; MORN; 7.
SMART; SM00698; MORN; 5.
                                                                                                                                                                      Local Similarity 37.5
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:12371; TSGA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
66
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                 301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meiosis; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
298
20
44
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                           TSA2 HUMAN
                     REPEAT
REPEAT
REPEAT
CONFLICT
                                                                                                               SEQUENCE
                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                      RESULT 11
TSA2_HUMAN
                                                                                                                                                                                         Matches
   FFFFFS
                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                           PHILL SAN THE 
                                                                                                                                                                                                                              6
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ### HOPPE-Seyler 376:617-625(1995).

-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: HYPHAL TIP.
-!- DEVELOPMENTAL STRAGE: EXPRESSED IN FILAMENTOUS DIKARYON.
-!- PTM: MAY ALSO BE O-GLYCOSYLATED.
-!- PTM: MAY BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cellulose degradation; Hydrolase; Glycosidase; Signal; Glycoprotein. SIGNAL 1 26 POTENTIAL. CHAIN 27 393 ENDOCTORTOLA. ACT STORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schauwecker F., Wanner G., Kahmann R.; "Filament-specific expression of a cellulase gene in the dimorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
8-FRB-2003 (Rel. 41, Last annotation update)
Endoglucanase 1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 1)
(Cellulase 1) (EG 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ustilago maydis (Smut fungus).
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 1; Length 393;
Pred. No. 17;
2; Mismatches 3; Indel8
                                                                                                                      DB 1; Length 309;
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY)
ALA/GLY/SER-RICH.
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LINKED (GLUNAC. . .) (PC 65C753C610CD6AD3 CRC64;
                                                                        09A20A766D5A6AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                   393 AA
                                                                                                                                                                        4; Mismatches
                                                                                                                            Score 45;
Pred. No.
MORN 4.
MORN 5.
MORN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S59499; SS9499.
HSSP; P43316; ZENG.
InterPro; IPR000334; Glyco_hydro_45.
Pfam; PF02015; Glyco_hydro_45; 1.
PROSITE; PS01140; GLYCOSYL_HYDROL_F4!
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96145728; PubMed=8590631;
112 MO
135 MO
181 MO
35124 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.7%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S81598; AAB36147.1; -.
                                                                                                                         35.7%;
                                                                                                                                                   46.78;
                                                                                                                                                                                                                           2 DLQERGDNDISPFSG 16
                                                                                                                                                                                                                                                        fungus Ustilago maydis.";
                                                                                                                                                   Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
152
385
```

유

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIAINS 21844401; PubMed=11859360;

WEDIAINS 21844401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros U., Peat N., Hayles J., Baker S., Basham D., Bewman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gonlins M., Connor R., Cronin N., Hurche E.J., Hunt S., Jagels K.,

Holroyd S., Horneby T., Howarth S., McDonald S., McLean J.,

Monory P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

An Mooney P., Moule S., Mangall K., Murphy L., Stevens K.,

An Intherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Taylor R.G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woltjens I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Egger P., Zimmermann W., Wedler H., Wambult R., Purnelle B.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Rominguez A., Revuelta J.L., Mooren S., Armstrong J., Forsburg S.L.,

Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.7%; Score 45; DB 1; Length 508; 64.3%; Pred. No. 23;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                     SEQUENCE OF 372-467 FROM N.A.
Chan S.Y., Delius H., Halpern A.L., Bernard H.U.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57827 MW; 3149549895534D00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetacese,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDBG_SCHPO STANDARD; PRT; 851 AA. 010366; 010-07-1996 (Rel. 34, Created) 01-077-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein C22E12.16c in chromosome I. SPACZ2E12.16C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002210; PV capsid L1.
Pfam; PF00500; late_protein L1; 1.
PRINTS; PR00865; HPVCAPSIDLI.
ProDom; PD000544; PV capsid L1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U31792; AAA79491.1; -. EMBL; U21876; AAA92837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coat protein; Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 DLQERFSNELSQFS 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 DLQERGDNDISPFS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
YDBG_SCHPO
       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDD TTDDDD TTDDDDD TTDDDDD TTDDDD TTDDDDD TTDDDD TTDDDD TTDDDDD TTDDDD TTDDD TTDDDD TTDDD TTDD TTD TTDD TTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 23844;
BEDINES-21092506; PubMed=2265762;
Tang L.B., Lenstra K., Borchert T.V., Vasantha N.;
"Isolation and characterization of levansucrase-encoding gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 96:89-91(1990).
-!- CATALYITC ACTIVITY: Sucrose + {(2,6)-beta-D-fructosyl}(N)
glucose + {(2,6)-beta-D-fructosyl}(N+1).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- INDUCTION: By sucrose.
-i- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.7%; Score 45; DB 1; Length 472; 45.0%; Pred. No. 21; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus amylolíquefaciens.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 60.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=40540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F38592D272677E7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLI HPV60 STANDARD; PRT; 508 AA. P5081; Q80947; 01-0CT-1996 (Rel. 34, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) Major capsid protein L1.
                                                                                                                                                                                                                                  472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Azzze, Jogosoz, Interproj. 100802. Interproj. 100802. Jogosoz, Glyco hydro 68. Pfam; PF02435; Glyco hydro 68; 1. Transferase; Glycosyltransferase; Signal. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 OKVGDNSIDSWKNAGRVFKD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 QERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus amyloliquefaciens.";
Gene 96:89-93(1990).
   235 QRKDDNTISPYSG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 45.0%
Best Local Similarity
Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Delius H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1390;
                                                                                                                                                                                                                                  BACAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                  SACB_BAC
P21130;
                                                                                                                                                     RESULT 13
SACB BACAM
SACB BACAM
DT 01-FEB DT 0
```

RESULT 14
VUL HPV60
VUL PPV60
DT P5082
DT 01-0C
DT 15-JU
DE Major
DE Major
CO Virus
OC Virus
OC NOBL
OX NCBL
OX NCBL
RR [1]
RP EDIU

엄

ઠે

ô

Gaps

ö

3; Indels

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7%; Score 45; DB 1; Length 851; Best Local Similarity 50.0%; Pred. No. 41; Matches 9; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A991F3C7E3D980BE CRC64;
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
-i- SIMILARITY: STRONG, TO YEAST PIKI.
-i- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SMO0146; PISAC; 1.
PROSTIE; PSO0915; PI3.4 KINASE 1; 1.
PROSITE; PSO0916; PI3.4 KINASE 2; 1.
PROSITE; PSS0290; PI3.4 KINASE 2; 1.
Hypothetical protein; Transferase; Kinase.
DOMAIN
581 827
PI3K/P14K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GeneDB_SPombe; SPAC22E12.16c; ...
InterPro; IPR000403; PI3 PI4 kinase.
PFam; PSR00454; PI3 PI4_Kinase; 1.
SMART; SM00146; PI3Kc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z70043; CAA93903.1; -. PIR; T38173; T38173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                RAH TARAH TA
```

Search completed: January 29, 2004, 12:39:09 Job time : 14.7105 secs

|:||: |||||: 382 TNLQDSTDNDISESESEG 399 1 TDLOERGDNDISPFSGDG 18

g

ð

Q810d5 uncultured Q81086 uncultured Q9c091 homo sapien

Ogyiga brucella me Ogkina brucella me Ogkina brucella me Oghio me

O8ZBM6 O8XRZ9 O8CP04 099TN0

092432 08B915 09F5V2 044497 09NK94 09KBJ7

Q8Y183 Q8FZN1

099738 mus musculu Q874v1 listeria mo Q9ndr9 branchiosto Q8vik4 mus musculu

Q9QY38 Q8Y4V1

Q9NDR9 Q8VIK4

Q8U6F1 Q8PKH6

033643

Q55321 Q8L0K0

```
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21309068; PubMed=11414762;
Argiro L., Desbarats M., Glorieux F.H., Ecarot B.;
Argiro L., Desbarats M., Glorieux F.H., Ecarot B.;
Mepe, the gene encoding a tumor-secreted protein in oncogenic hypophosphatemic osteomalacia, is expressed in bone.";
Genomics 74:342-351(2011).
EMBL; AJ276396; CAB97250.1; -.
EMBL; AF325916; AAK70343.1; -.
EMBL; AF325916; MEPE.
Signal.

1 7 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Bone;
MEDINE=20399567; PubMed=10945470;
MEDINE=20399567; PubMed=10945470;
ECONS M.J., Oudet C.L.; P.A., Dong R., Wang H.R., White K.E.,
"MEDE, a new gene expressed in bone marrow and tumors causing osteomalacia.",
Genomics 67:54-68(2000).
                                                                                                                                                                                                                                                                                                                                                                                                    01-07T-2000 (TrEMBLrel. 15, Created)
01-07T-2000 (TrEMBLrel. 15, Last sequence update)
01-07T-2002 (TrEMBLrel. 22, Last annotation update)
Matrix extracellular phosphoglycoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525 M
58419 MW;
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
18
 CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             RESULT 1
  29NQ7
                                                                                                                                                                                                                                                                                                                                                                                              Q95kg5 macaca fasc
Q9n076 macaca fasc
Q9m076 macaca fasc
Q924il mus musculu
Q98416 mus musculu
Q8k16 mus musculu
Q8k3v0 rattus norv
Q8nc19 homo sapien
Q81up7 homo sapien
Q52676 rhodobacter
Q810m4 uncultured
Q8ebb9 shewanella
Q9evyO drosophila
Q8nyl corypabacte
Q81016 uncultured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29nq76 homo sapien
                                                                        January 29, 2004, 12:35:53; Search time 33.8947 Seconds (without alignments) 175.107 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                              830525
            5.1.6
Compugen Ltd
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                          830525 segs, 258052604 residues
            GenCore version (c) 1993 - 2004
                                                                                                                US-09-812-485A-49
126
1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                             SPTREMBL 23:*

1: SP_archea!*

2: Sp_bacteria:*

3: Sp_lungi:*

5: Sp_lungi:*

5: Sp_lungi:*

6: Sp_lungi:*

7: Sp_lungi:*

8p_organolle:*

8p_organolle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0990Q76
095KGS
0900X6
092411
092411
09830
08K4L6
08K4L6
08K10
08K10
08K10
08C19
08C19
08C19
08C19
08C19
08C19
08C19
08CH8
                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 2 2 2 2 2 2 4 2 9 2 4 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>DB</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2443
2423
320
3356
3356
339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555
555
433
435
                     Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1123
11233
11233
11233
881
881
881
890
502
503
503
64
499
699
                                                                                                                                                            Scoring table:
                                                                                                                            Perfect score:
                                                     OM protein -
                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                                                                          Searched:
                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                          Database
                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
```

525 AA

ALIGNMENTS

POTENTIAL,
MATRIX EXTRACELLULAR PHOSPHOGLYCOPROTEIN,
0977CA6E871CA9E5 CRC64;

Score 126; DB 4; Length 525; Pred. No. 7.8e-11;

Matches

셤

ò

```
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATRIX EXTRACELLULAR PHOSPHOGLYCOPROTEIN. 7CD603CAA8CB41B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                       Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Wakaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050259; BABJ7010.1; -.
SEQUENCE 555 AA; 61950 MW; BD4D47E88038A9E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J;
MEDLINE=21309068; PubMed=11414762;
Argiro L., Desbarats M., Glorieux F.H., Ecarot B.;
Nepe, the gene encoding a tumor-secreted protein in or hypophospharemic osteomalacia, is expressed in bone.";
Genomics 74:342-351(2001).
EMBL; AF314964; AAK70342.1;
                                                                                         01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Marrix extracellular phosphoglycoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 123; DB 6;
Pred. No. 2.4e-10;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.3%; Score 81; DB 11; 75.0%; Pred. No. 0.00049;
                                               555 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 TDLOERGDNDMSPFSGDGQPFKD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TDLOERGDNDISPFSGDGOPFKD 23
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 DLLVRGDNDVPPFSGDGQHF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DLQERGDNDISPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 M
45984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 97.6%;
Local Similarity 95.7%;
les 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 75.0 les 15, Conservative
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:2137384; Mepe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
19 4
433 AA;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxiD=10090;
                                                                                                                                                                                                                                                                                        NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                    MEPE protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               092411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ES02
                                               09GM13
RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
                      29GM13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ES02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Temporal cortex;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoro K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 55.6 kDa protein.
Hypothetical 55.6 kDa protein.
Hypothetical 55.6 kDa protein.
Bacaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matrix extracellular phosphoglycoprotein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 123; DB 6; Length 555;
Pred. No. 2.4e-10;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 500;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              libraries.", Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB060891; BAB46894.1; -. Hypothetical protein. SEQUENCE 500 AA; 55577 MW; 918D265AD8EDC7BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046056; BAB01638.1; -.
SEQUENCE 555 AA; 61979 MW; CCFE1A98ADA19EE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.6%; Score 123; DB 6;
95.7%; Pred. No. 2.1e-10;
                                                                                                                                                                                                                     500 AA.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDLQERGDNDMSPFSGDGQPFKD 240
                                                                                  TDLQERGDNDISPFSGDGQPFKD 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOLOERGDNDMSPFSGDGQPFKD 295
                                                 1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.7°
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
  Conservative
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
22; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9541;
  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            970N69
```

RESULT 3

g

900N60

a

ö

Gaps

ö

Length 555;

ô

Gaps

. 0

Indels

Length

in oncogenic

```
Q8K3V0;

Q1-OCT-2002 (TEMBLrel. 22, Created)

O1-OCT-2002 (TEMBLrel. 23, Last sequence update)

O1-MAR-2003 (TEMBLrel. 23, Last annotation update)

Osteoregulin-like protein.

Osteoregulin-like protein.

Matura norvegicus (Rat).

Bukaryota; Metazos; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                           Wang X., Hu B., Wang Y.;
"Rattus norvegicus cDNA sequence expressed in B4 cell line (possible subtype of osteoregulin).";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS10559; AAM94401.1; -.
SEQUENCE 443 AA, 47672 MW; 720EEC4C0718FB14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamaro J., Wakamatau A., Makamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Susaki N., "NEDO human DNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                    64.3%; Score 81; DB 11; Length 443; 75.0%; Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 80; DB 4; Length 275; 93.8%; Pred. No. 0.00042; ive 0; Mismatches 1; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 AA; 31358 MW; AF0B426A671B665C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
10-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ90595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 DLLVRGDNDVPPFSGDGOHF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DLQERGDNDISPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TDLQERGDNDISPFSG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBIUP7;
01-MAR-2003 (TYEMBLYEL. 23,
01-MAR-2003 (TYEMBLYEL. 23,
01-MAR-2003 (TYEMBLYEL. 23,
Similar to phospholipase B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
wes 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
                                                                                                                                                                                                                                                               STRAIN=F344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBNC19
QBNC19;
Q8K3V0
ID Q8K3V0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8IUP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
Q81UP7
ID Q81UP
AC Q81UP
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBNC19
                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hattus norvegicus CDNA sequence highly expressed in Al-5 cell line (identical to osteoregulin) "; Submitted (JUL-2002) AAG33366.1; -. EMBL/GenBank/DDBJ databases. EMBL, AF530558; AAM94403.1; -. SEQUENCE 435 AA; 46515 MW; D587F82968A26BCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gowen L.C., Petersen D.N., Vail A.L., Stock J., Tkalcevic G.T., Simmons H.A., Chidsey-Frink K.L., Ke H., McNeish J., Brown T.A.; "Targeted disruption of the osteoregulin gene results in increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                              SEGUENCE FROM N.A.
STRALNE-Spraque-Dawley;
MEDLINE-20549633; PubMed-10967096;
Petersen D.N., Tkalcevic G.T., Mansolf A.L., Rivera-Gonzalez R.,
                                                                                                                                                                                                                                                                             Brown T.A.;
"Identification of Osteoblast/Osteocyte Factor 45 (0F45), a Bone specific cDNA Encoding an RGD-containing Protein That Is Highly Expressed in Osteoblasts and Osteocytes.";
J. Biol. Chem. 275:36172-36180(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.3%; Score 81; DB 11; Length 435; 75.0%; Pred. No. 0.0005; 4; Indels arive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.3%; Score 81; DB 11; Length 441; 75.0%; Pred. No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF298661; AAM87687.1; -.
MGD; MGI:2137384; Mepe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 AA; 46872 MW; AA1947BFE9F2E300 CRC64;
                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DLQERGDNDISPFSGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DLQERGDNDISPESGDGQPF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                 Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone density."
                                                                              Osteoregulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osteoregulin.
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=F344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08K4L6
08K4L6;
```

ö

Gaps

ö

Matches

ö

Gaps

ö

```
52.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY_2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14, CG14085 protein.
EMBL; AB085239; BAB96823.1;
                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shewanella oneidensis.
                                                                                                                    1
356 3
356 AA;
                                                                                                                                                                                                                                                              Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                      Ligase.
NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8EHB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09VVY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
QBEHB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
     SO FF FW DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDT TO DD T TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97149280; PubMed=8996088;
Trieschmann M.D., Pattus F., Tadros M.H.;
"Molecular characterization and organization of porin from Rhodobacter
capsulatus strain 3784.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Matsui H., Tajima K., Ogata K.;
"Diversities of Formyltetrahydrofolate Synthetase Genes Recovered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; DB 2; Length 320;
Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                        Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC042674; AAH42674.1; -SEQUENCE 423 AA; 47354 MW; A20A193491BA780C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0cr-2002 (TrEMBLrel. 22, Created)
01-0cr-2002 (TrEMBLrel. 22, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
putative formylterrahydrofolate synthetase (EC 6.3.4.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rumen Contents.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEML, U57653; AAB41301.1; -.
HSSP; P31243; 2POR.
SEQUENCE 320 AA; 33396 MW; B0E1745CB9D86F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PORCA.
Rhodobacter capsulatus (Rhodopseudomonas capsulata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 AA.
                                                                                                                                                                                                                                                                                                                                                                                9.4;
                                                                                                                                                                                                                                                                                                                                                     42.1%; Score 53; DB 52.2%; Pred. No. 9.4; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | | | | | : : | | | | TPLNERGDTDLTFFSEDCFHFSD 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TDLQERGDNDISPFSGDGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uncultured bacterium.
Bacteria, environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| :|| |||
TDLDDRGGNDIPYLTGD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDLQERGDNDISPFSGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.3%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 52.2
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity ?
     sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 183:61-68(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                  SEQUENCE FROM N.A
                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1061;
                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       052676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBLOM4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8L0M4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            052676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
081.0M
AC 081.0M
AC 081.0M
DT 01-0C
DT 01-M
DE (Prag
OS Uncul
OC Bacte
OX NCBI
RP SEQUE
RR MATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
052676
DD 01-NO
DT 01-NO
DT 01-NO
DD 01-NO
DD NOL-NO
RT CAPAI
     SOCOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Taspin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 1007; 71;
                                                                                                                                                                                  DB 2; Length 356;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 1007 AA; 110092 MW; 8123B725E2CE61F2 CRC64;
                                                                                                            356
38922 MW; 485E9F884AC9FD43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1007 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    793 AA
                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                           39.7%; Score 50; 42.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.7%; Score 50; 52.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015574; AAN54374.1; -.
Interpro, IPR000559; Fmtethyd_synth.
Pfam; PF01268; FTHFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                    80 DLQDRIENILLGITSDGKPFR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565 TOKAMRGDAITFNDVPPFEGD 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                     2 DLQERGDNDISPFSGDGQPFK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TDLQERGD----NDISPFSGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conserved hypothetical protein. SO1309.
```

```
RN [1]

RD SEQUENCE FROM N.A.

RADIAN=BERKELER!

RA Addans W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addans W.D., Celniker S.E., Holt R.A., Farburner M., Henderson S.N.,

RA Addans W.D., Celniker S.E., Holt R.A., Farburner M., Henderson S.N.,

Sutton G.G., Wortman J. R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peieiffer B.D.,

RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peieiffer B.D.,

RA Ballew R.M., Basu A., Baxten E.G., Helt G., Walson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxten E.G., Helt G., Walson C.R., Miklos G.L.G.,

RA Beeson K.Y., Berman B.P., Bhandari D., Bolshakov S.,

RA Beeson K.Y., Busem D.A., Butler H., Cadieu E., Center A., Chandre I.N.,

RA Butris K.C., Berman B.P., Bhandari D., Bolshakov S.,

RA Butris K.C., Berman B.P., Bhandari D., Bolshakov S.,

RA Butris K.C., Bermen B.P., Butler H., Cadieu E., Center A., Dietz S.M.,

RA Butris K.J., Evangelista C.C., Ferract C., Ferract S., Dunkov B.C., Dunn P.,

RA Dodson K., Doug L.E., Gornell J.H., Gu Z., Glabart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glabart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heilman T.J., Well M.-H., Ibegwan C.,

RA Harris N.L., Harvey D., Halman T.J., Well M.-H., Ibegwan C.,

RA Lasko P., Lei Y., Leviteky A.A., Li J. J., Li Z., Liang Y., Lin X.,

Rakopel B.L., Molton K.A., Nixon K., Nusskern D.R., Moshrefi A.,

Rakopel B.C., Siden Klang G.S., Rang R., Sun B.,

Rainer B.C., Siden Klang G., Milbina N., Stunder R., Wang X.,

Rang Z.-Y., Mestender D.A., Nixon K., Nusskern D.R., Wang X.,

RA Buter S. M., Moy M., Winder S., Calbard J., Weissenberh J.,

RA Buter S. M., Woodage T., Worley K.C., Wu Sissenberh J.,

RA Sheng R., Reiner R., Rubin G.M., Venter E., Wang S., Yao O., Zheng L.,

RA Sheng R.H., Zhong F.N., Zhong W., Zhan S., Zhon S., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.3%; Score 49.5; DB 5; Length 793; 61.1%; Pred. No. 65; ive 1; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL. AE001517; AAF49175.1; -.
FlyBase; FBGN0036859; CG14085.
SEQUENCE 793 AA; 88674 MW; FFC0E3DF3E537C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2002 (TrEWBLrel. 22, Created)
01-0CT-2002 (TrEWBLrel. 22, Last sequence update)
01-0CT-2002 (TrEWBLrel. 22, Last annotation update)
Hypothetical protein Cgl1322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             693 GDNDPSPFQGIQGQNIKE 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 GDNDISPFSG-DGQPFKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBNOVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
008NQV1
1D Q8NOV
AC Q8NOV
DT 01-0C
DT 01-0C
DT 01-0C
DE Hypor
CGL13
CGCN
OC COCYN
OX NCBL
RP SEQUE
RR STRAI
RC STRAI
RC
                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
```

```
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AP005278; BAB98715.1; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 326 AA; 34230 MW; 9D56CD723867D686 CRC64;

Query Match

Query Match

Best Local Similarity 40.0%; Pred. No. 29;

Matches 10; Conservative 3; Mismatches 4; Indels 8; Gaps

Qy 5 ERGDNDISPFSG------DGQPF 21

| | | | | | | | | | | | |

DD 163 DSADNPVAPFSSAVDKLEKRDGQPF 187
```

Search completed: January 29, 2004, 12:40:18 Job time : 34.8947 secs THIS PAGE BLANK (USPTO)

```
02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU93724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU93724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 January 29, 2004, 12:34:18; Search time 28.0263 Seconds (without alignments) 84.952 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107863
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                     1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                US-09-812-485A-47
82
                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                  OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                             Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					COLUMNITO	
		æ				
Result		Query				
Q	Score	Match	Match Length DB ID	98	ID	Description
-				;	AATTO2424	10 1 10 10 10 10 10 10 10 10 10 10 10 10
4	30			3	F7/020W	הפוורמז הזסמתר הסוו
8	82	100.0	15	23	AA020377	C-terminal amidate
m	82	100.0	23	23	AAU93726	Dental product bon
4	82	100.0	23	23	AA020379	C-terminal amidate
ហ	82	100.0	97	23	AAU93681	Dental product bon
9	82	100.0	97	23	AA020331	Protein of matrix
7	82	100.0		21		Amino acid sequenc
60	82	100.0	430	22		Truncated phosphat
σ	R2	0 00 0		22		Himan Oateoregilin

Human osteoregulin Phosphatonin polyh Human phosphatonin Human oncogenic os Human osteoregulin Human osteoregulin	n of mat COM1 cal teoregul costeoreg e of a c product product e of mat		
AAB62920 AAB62689 ABB08526 AAE13227 AAB82923 AAB82921	AAO20353 AAE13130 AAE82918 AAB82918 AAO20372 AAO20378 AAO20370 AAO20360 AAO303507	AAO20376 AAU33704 AAU33705 AAU93705 AAO20356 AAO20356 AAO20356 AAO12478 ABG08384 AAU154077 ABG10214 AAU15962626 AAE10214 AAO1956 AAE2860	ALIGNMENTS
2223322	222222222222	353555555555555555555555555555555555555	
222222 22222 22222 22225 2025	2 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	115 400 400 330 330 330 101 101 103 103 103 103 1	
	933 933 935 937 937 937 937 937 937 937 937 937 937	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	
885 42 43 43 43 43 43 43 43 43 43 43 43 43 43	77777777777777777777777777777777777777	44 44 4 0	
011111	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic. Dental product bone growth enhancing peptide #44. AAU93724 standard; peptide; 15 AA. (first entry) WO200213775-A1. 21-FEB-2002.

Kumagai Y; 09-AUG-2001; 2001WO-US25101 16-AUG-2000; 2000US-225879P (BIGB-) BIG BEAR BIO INC. Nomizu M, WPI; 2002-329525/36. Yoneda T,

Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific

```
The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of esteoblast or odnitoblast cells on the surface of the new skeletal growth. AAU933681-AAU93726 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
                                                                                                                                                                                                                                                                                                              ö
amino acid in a sequence containing the integrin binding motif
                                                                                                                                                                                                                                                                              Length 15;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                              Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                               100.0%; Score 82; DB 23; 100.0%; Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal amidated synthesised peptide D-00004.
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoneda T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 23; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAO20377 standard; peptide; 15 AA.
                                Claim 12; Page 21; 44pp; English
                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2001; 2001WO-US25542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000; 2000US-0641034.
19-MAR-2001; 2001US-0812485.
                                                                                                                                                                                                                                                                                                                                                                FRGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                        1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                              Local Similarity 100.
es 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIGB-) BIG BEAR BIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-291971/33.
                                                                                                                                                                                                                                                 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            weakness; D00004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200214360-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kumagai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                   AA020377
                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                           8
```

The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
motif and a calcium binding motif. The peptide of the invention is useful
             for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts /osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a C-terminal amidated synthesised peptide D-00004 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of esteoblast or dontoblast cells on the surface of the new skeletal growth. AAU33681-AAU33726 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dental product useful for treating skeletal diseases e.g. dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                        100.0%; Score 82; DB 23; 100.0%; Pred. No. 4.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dental product bone growth enhancing peptide #46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
6.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 82; DB Best Local Similarity 100.0%; Pred. No. 6.8e Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                AAU93726 standard; peptide; 23. AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumagai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 21; 44pp; English.
                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001; 2001WO-US25101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000; 2000US-225879P
                                                                                                                                                                                                                                                                                                       1 ERGDNDISPFSGDGQ
                                                                                                                                                                                                                                               15; Conservative
                                                                                                                                                                                                                                                                                    1 ERGDNDISPFSGDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIGB-) BIG BEAR BIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-329525/36
                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                     15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200213775-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoneda T,
                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                               AAU93726
8888888888888
                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                     g
```

```
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO20331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
AAU93681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA02033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts for secondarion associated with skeletal loss or weakness. This sequence represents a C-terminal amidated synthesised
                                                                                                                                                                        Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                     C-terminal amidated synthesised peptide D-00006.
                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 15; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Yoneda T;
                                                                                    AAO20379 standard; peptide; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide D-00006 of the invention.
                                                                                                                                                                                                                                                                                                                                             14-AUG-2001; 2001WO-US25542.
                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2000; 2000US-0641034
19-MAR-2001; 2001US-0812485
           ERGDNDISPESGDGO 15
                            5 ERGDNDISPFSGDGQ 19
                                                                                                                               31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   (BIGB-) BIG BEAR BIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                       Blacher RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-291971/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 AA;
                                                                                                                                                                                                            weakness; D00006.
                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                 WO200214360-A1
                                                                                                                                                                                                                                                                                                                        21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       Kumagai Y,
                                                                                                                                                                                                                                 Synthetic.
                                                                                                           AA020379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                RESULT
                                                                                      ò
                           유
```

ß

a

RESULT 5

ERGDNDISPESCOCO 15

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of osteoblast or odontoblast cells on the surface of the new skeletal growth. AAU93681-AAU93726 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; weakness; matrix extracellular phosphoglycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein of matrix extracellular phosphoglycoprotein containing RGD #1.
                                                                                                                                                                                                                            Dental product; toothpaate; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 82; DB 23; Length 97; 100.0%; Pred. No. 3.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                       Dental product bone growth enhancing peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 11; 44pp; English
Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO20331 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoneda T, Nomizu M, Kumagai Y;
AAU93681 standard; protein; 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001; 2001WO-US25101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-2000; 2000US-225879P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIGB-) BIG BEAR BIO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-329525/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   WO200213775-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-2002
                                                                                                                  02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XXXXXXXXXXXXXXXXX
```

WO200214360-A1

21-FEB-2002.

Unidentified

(BIGB-) BIG BEAR BIO INC. Y, Blacher RW,

WPI; 2002-291971/33

Kumagai

```
423..426
/note= "Casein kinase II phosphorylation site"
425..428
/note= "protein kinase C phosphorylation site"
                             "Casein kinase II phosphorylation site"
                                                                                                                                "protein kinase C phosphorylation site"
                                                                                                                                                                 "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                    "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..231
te= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                  note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                    "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "protein kinase C phosphorylation site"
325..328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "cAMP and cGMP dependent protien kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "protein kinase C phosphorylation site"
                                                                                               "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                  i..165
ote= "glycosaminoglycan attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                  "cell attachment tripeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amidation site"
382..386
/note= "Asu-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Asu-glycosylation site"
384..386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "myristoylation site"
                                                                                                                                                                                                                                                                    "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "myristoylation site"
                                                                "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "p
224..227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "p
312..314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "p
315..320
                                                                                                                                                                                                                                                                                    .154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228..230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .408
                                                                                                                                                                                                                                                   143..148
                                                                                                                                                                                                                                                                                                                                                                                                                   199..202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .394
                                                                                                                                                   118..120
                                                                                                                                                                                                                    139..142
                                                                                                                                                                                                                                                                                                                                                   177..180
                                                                                                                                                                                                                                                                                                                                                                                      194..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                      203..205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311..313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319..321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370..373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103..405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .410
                                                                                                                                                                                   119..224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238..241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109..411
                                                                                40..47
/note=
                                                                                                                                                                                                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                 'note=
                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                  'note=
                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                 Modified-site
                                              Modified-site
                                                                                Modified-site
                                                                                                               Modified-site
                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andified-site
                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                     Region
 ö
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a protein of a matrix extracellular phosphoglycoprotein containing an RGD motif of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEPE; Na+-dependent phosphate cotransport; vitamin D metabolism; bone mineralisation; phosphate metabolism related disease; hyperphosphatemia; renal osteodystrophy; renal dialysis; secondary hyperparathyrodism; osteitis fibrosa cystica; hypercalcuria; X-linked hypophosphatemic ricket; hereditary hypophosphatemic ricket; hereditary hypophosphatemic ricket; hereditary hypophosphatemic ricket; oncogenic hypophosphatemics osteomalacia; renal phosphate leakage; neceditary hypothospia; osteoporosis; vitamin D resistant rickets; end organ resistance; renal Fanconi syndrome; autosomal rickets; paget's disease; kidney failure; renal tubular acidosis; sprue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphatonin; Metastatic-tumour Excreted Phosphaturic-Element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                  New peptide compound useful for reducing bone loss, is capable enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human phosphatonin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82; DB 23;
Pred. No. 3.5e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY53812 standard; Protein; 430 AA.
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 11; 50pp; English
                                                                                                                                                                                                                    Ë
                                                                                                                                                                                                                    Yoneda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                 14-AUG-2001; 2001WO-US25542
                                                                                                                                16-AUG-2000; 2000US-0641034
19-MAR-2001; 2001US-0812485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ERGDNDISPFSGDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERGDNDISPESGDGO
```

97 AA

Sequence

47

8 음 Key Modified-site

Homo sapiens

22-FEB-2000

Human;

AAY53812;

S

Rowe P;

Nev

```
/note= "the amino acid residues in this region are indicated incorrectly in the sequence provied in the sequence listing"
                     Key Location/Qualifiers Misc-difference 161..192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB82922 standard; Protein; 509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 8; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 ERGDNDISPFSGDGQ 165
                                                                                                                                                                                                                                                     99US-0434185.
99GB-0026424.
                                                                                                                                                                                                                 31-OCT-2000; 2000WO-EP10747
                                                                                                                                                                                                                                                                                                             (UNICO ) UNIV COLLEGE LONDON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
Hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-343487/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF83759
                                                                                                                                       WO200132878-A2
                                                                                                                                                                                                                                                     04-NOV-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-2001
                                                                                                                                                                           10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB82922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                     Rowe P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a phosphatonin polypeptide (also called Metastatic-tumour Excreted Phosphaturic-Element (MEPE)). The level of phosphatonin in a subject modulates Na+dependent phosphate octransport, vitamin in metabolism and/or bone mineralisation. The phosphatonin polypeptides, polynucleotides, weetors and antibodies are used to treat phosphatemia, or renal osteodystrophy, hyperphosphatemia in renal dialysis/pre-dialysis, secondary hyperparathyrodism or osteitis fibrosa cystica, or X-linked hypophosphatemic rickets, hereditary hypophosphatemic rickets with hyperparathyrodism or osteitis fibrosa cystica, or X-linked hypophosphatemic rickets, hereditary hypophosphatemic costeomalacia, renal phosphate lessage, renal costeodystrophy, osteomalacia, renal phosphate lessage, renal osteodystrophy, osteoporosis, vitamin D resistant rickets, end organ resistance, renal receptores, autosomal rickets, paget's disease, kidney failure, renal tubular acidosis, cystic fibrosis or sprue. The polypeptide may also be used to manufacture combined preparations for simultaneous, dispraders a transformed cerealment of phosphate metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metastatic-tumour excreted phosphaturic element; MEPE; phosphatonin; phosphate; vitamin-D; skeletal formation; mineralization; truncated; osteopathic; antigout; cytostatic; human.
                                                                                                                                                                                                                                                                                                                                                                                       polypeptides involved in the regulation of phosphate metabolism ful for diagnosing and treating disorders related to phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders. A transformed osteoblast or bone cell line capable of phosphatonin overexpression is useful for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
/note= "Casein kinase II phosphorylation site"
427..430
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 82; DB 21; Length 430; 100.0%; Pred. No. 2e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Truncated phosphatonin polypeptide (truncated MEPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB62669 standard; Protein; 430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Fig 8; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0010681.
98GB-0019387.
                                                                                                                                                           99WO-EP03403
                                                                                                                                                                                                                                                   (UNLO ) UNIV COLLEGE LONDON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                               WPI; 2000-053262/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 AA;
                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ36447
                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphatonin.
                                                                                                                                                         18-MAY-1999;
                                                                                                                                                                                                                 04-SEP-1998;
                                                                               WO9960017-A2
                                                                                                                                                                                             18-MAY-1998;
                                                                                                                   25-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB62669;
                                                                                                                                                                                                                                                                                                                                                                                                                               metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
```

```
The invention relates to a novel human protein, metastatic-tumour excreted phosphaturic element (MEPE) or phosphatonin (modulator of phosphaturic element (MEPE) or phosphatonin (modulator of phosphate and vitamin-D metabolism). The phosphatonin polypeptides, of its of the phosphate or vitamin D metabolism, skeletal formation and mineralization. Phosphatoning are used to treat hyperphosphatemia, renal cetodystrophy, secondary hyperparathyroidism, ostatis fibrosa cystica or gout. It is used to prepare a medicament for treating X-linked hyperposphatemic rickets, hereditary hypophosphatemic rickets hereditary hypophosphatemic rickets hereditary hypophosphatemic rickets hereditary hypophosphatemic rickets and hypercalcuria (HHRH), hypomineralized bone lesions, stunted growth in juveniles, oncogenic hypophosphatemic osteomalacia, renal phosphate ced organ resistance, renal tubular acidosis, cystic fibrosis or disease, kidney failure, renal tubular acidosis, cystic fibrosis or express Phosphatonin golymucleotides are useful as molecular weight markers on Southern gels, as diagnostic probes for detecting the presence of a specific markers on southern gels, as diagnostic probes for detecting the presence of a specific markers on southern gels, as diagnostic probes are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
New phosphatonin polypeptide a regulator of phosphate metabolism, for diagnosing and treating disorders of phosphate, vitamin-D metabolism, skeletal formation e.g. osteoporosis, Paget's disease, gout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying agonists and antagonists, compounds which bind to phosphatonin and drug candidates for therapy of phosphate metabolism disorders. The present sequence represents a truncated form of phosphatonin (MBPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osteoregulin; human; bone; homeostasis; adipose; calcification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 82; DB 22; Length 430; 100.0%; Pred. No. 2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human osteoregulin (mature polypeptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXEXEXEX
```

Query Match

Matches

ò 셤 Homo sapiens

Homo sapiens. EP1130098-A2

therapy.

05-SEP-2001

Brown TA,

```
The present sequence is that of human osteoregulin, a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. The sequence is predicted from the nucleotide sequence (see AAM26808) of isolated osteoblast cDNA. A splice variant of human osteoregulin was also cantibodies, host cells incoming provides novel animal cells and mammals with express heterologous osteoregulins, and animal seminal arrayeted disruption of an animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with content of the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metastatic-tumour excreted phosphaturic element; MEPE; phosphatonin; phosphate; vitamin-D; skeletal formation; mineralization; truncated; osteopathic; antigout; cytostatic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 82; DB 22; Length 525; 100.0%; Pred. No. 2.5e-05; ive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                          Gowen LC, Hames LM;
                              1..37
/label= Signal_peptide
38..525
                                                                                     /label= Mature protein
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 45-47; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB62689 standard; Protein; 525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphatonin polypeptide (MEPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERGDNDISPFSGDGQ 260
                                                                                                                                                                                                                                                                        29-FEB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
                                                                                                                                                                                                                                27-FEB-2001; 2001EP-0301768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                          Brown TA, De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-604111/69.
N-PSDB; AAH26808.
                                                                                                                                     EP1130098-A2
                                                                                                                                                                                  05-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB62689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
  Key
Peptide
                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of human osteoregulin mature polypeptide, i.e. lacking an N-terminal signal sequence.
Colstoorgulin is a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. 2 Splice variants of human osteoregulin were identified (see also AAB82923). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, animal reals and mammals with a targeted disruption of an animal real mammals with a targeted disruption of an osteoregulin gene. The invention provides screening asseys to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with osteoregulin activity. The modulators of activity may be useful in the manufacture of a medicament for, as well as for treating, ammmal in need of regulation of bone mass and/or density, adiposity, vacular flexibility, and/or atherosclerotic plaque calcification contential pone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel osteoregulin polypeptide useful for regulating bone homeostasis,
  atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osteoregulin, human; bone; homeostasis; adipose; calcification; atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adiposity and calcification of atherosclerotic plagues comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 82; DB 22;
100.0%; Pred. No. 2.4e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Hames LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measuring the activity of osteoregulin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 54-55; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB82920 standard; Protein; 525 AA.
                                                                                                                                                                                                                                                                                                                                                                       Gowen LC,
                                                                                                                                                                                                          27-FEB-2001; 2001EP-0301768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 ERGDNDISPESGDGQ 244
                                                                                                                                                                                                                                                     29-FEB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERGDNDISPFSCDGQ
                                                                                                                                                                                                                                                                                                                        (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                       De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-604111/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human osteoregulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH26810.
```

ö

Gaps

ö

Homo sapiens

21-DEC-2001

AAB82920;

RESULT 10 AAB82920

8 g

Sequence

Homo sapiens

therapy

Rowe

```
This invention relates to human phosphatonin which has the activity of lowering blood phosphate and increasing urinary phosphate. The proteins are cytostatic, antidiabetic and antiinflammatory in their action. Phosphatonin down-regulates sodium-dependent phosphate transport in the kidney, it down-regulates 55-hydroxy-aitamin D3-1alpha-hydroxylase in the kidney, if down-regulates 55-hydroxy-aitamin D3-24-hydroxylase in the kidney. Phosphatonin seful in the diagnosis, treatment and prevention of phosphate metabolism related diseases such as hyperphosphaemia, arteriosclarosis, heart failure, diabetic renal disease, kidney failure, acute coronary disease and cystic fibrosis. This sequence represents human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signal_peptide
17..525
/note= "Mature oncogenic osteomalacia-related protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; oncogenic osteomalacia-related protein 1; 00M1; gene therapy; phosphate homeostasis-related disease; rickets; osteomalacia; cardiant; rhabdomyolysis; cardiomyopathy; tumoural calcinosis; renal failure; bone mineralisation; phosphaturia; cellular process.
                                                                                                                                                                                                                                                                                                 Phosphatonin of human origin and DNA encoding it for diagnosis and treatment of diseases associated with disorders of phosphate metabolism, e.g., hyperphosphaemia, arteriosclerosis, heart failure, diabetic renal disease and kidney failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human oncogenic osteomalacia-related protein-1, (OOM-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 82; DB 23;
100.0%; Pred. No. 2.5e-05;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235..258
/note= "Calcium binding motif"
247..249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Calcium binding motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                          Morimoto S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE13227 standard; Protein; 525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1-4; 130pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 ERGDNDISPFSGDGQ 260
                                                              20-JUN-2001; 2001WO-JP05263
                                                                                                         21-JUN-2000; 2000JP-0191088
                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ERGDNDISPESCOGO 15
                                                                                                                                                                                                                                      WPI; 2002-139791/18.
N-PSDB; ABA99159, ABA99160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OOM-1) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130..142
                                                                                                                                                                                            Yamada T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-2002
                                                                                                                                                                                          Kurokawa T,
                      27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE13227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE1322
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel human protein, metastatic-tumour excreted phosphaturic element (MEPE) or phosphatonin (modulator of phosphate and vitamin-D metabolism). The phosphatonin polypeptides, polymucleotides and specific antibodies are useful for treating a disorder of phosphate or vitamin D metabolism, skeletal formation and mineralization. Phosphatonins are used to treat hyperphosphatemia, renal osteodystrophy, secondary hyperparathyroidism, osteitis fibrosa cystica or gout. It is used to prepara medicament for treating X-linked or ypophosphatemic rickets, hereditary hypophosphatemic rickets with hypophosphatemic rickets with hypophosphatemic rickets with hypophosphatemic osteomalacia, renal posteodystrophy, osteophosphatemic rickets, renal costeodystrophy, osteophosphatemic rickets, paget's classas, kidney failure, renal tubular acidosis, vitamin-D resistant rickets, end organ resistance, renal tubular acidosis, cystic fibrosis or cystic fibrosis or sprue. Phosphatonin polymucleotides are useful as molecular weight capruse. Phosphatonin polymostic probes for detecting the presence of assess and antegonists, compounds which bind to phosphatonin and drug candidates for therapy of phosphate metabolism disorders. The present sequence represents the amino acid sequence of the entire phosphatonin (MEPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                  New phosphatonin polypeptide a regulator of phosphate metabolism, for diagnosing and treating disorders of phosphate, vitamin-D metabolism, skeletal formation e.g. osteoporosis, Paget's disease, gout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human phosphatonin; cytostatic; antidiabetic; antiinflammatory; hyperphosphaemia; arteriosclerosis; heart failure; diabetic renal disease; kidney failure; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 82; DB 22;
100.0%; Pred. No. 2.5e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 133-134; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB08526 standard; protein; 525 AA.
                                                                                                                                                   99US-0434185.
99GB-0026424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 ERGDNDISPFSGDGQ 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                (UNLO ) UNIV COLLEGE LONDON
                                                                                                         31-OCT-2000; 2000WO-EP10747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-343487/36.
N-PSDB; AAF83764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human phosphatonin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 AA;
                      WO200132878-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200198495-A1
                                                                                                                                                   04-NOV-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                 10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB08526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                             ä
```

셤 ð

ö

Gaps

ö

Length 525; Indels

```
Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin -
                                                                                                                                                      Osteoregulin, human, bone, homeostasis, adipose, calcification, atherosclerosis, osteoporosis, osteopathic, antiarteriosclerotic,
                                                                                                                  Human osteoregulin (mature polypeptide)
AAB82923 standard; Protein; 540 AA.
                                                                                                                                                                                                                                                                                                                                                                                      29-FBB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
                                                                                                                                                                                                                                                                                                                                                  27-FEB-2001; 2001EP-0301768
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown TA, De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-604111/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH26811
                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                      EP1130098-A2
                                                                            21-DEC-2001
                                                                                                                                                                                                                                                                                                              05-SEP-2001
                                      AAB82923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
AAB82921
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designated COM1 (oncogenic osteomalacia-related factor) and its DNA molecule. COM1 protein is useful for treating a phosphate homeostasis-related disease such as X-linked hypophosphatemia rickets, oncogenic osteomalacia, rhabdomyolysis, cardiomyopathy, tumoural calcinosis and renal failure. OOM1 proteins and DNA's are useful for modulating the phenotype of a neoplastic cell associated with oncogenic osteomalacia; modulating bone mineralisation; and treating a disease characterised by abnormal bone mineralisation; and treating an oncogenic osteomalacia. Concentrations of 1,25-dihydroxy vitamin Dor osteomalacia. OOM is useful for modulating renal phosphate transport, which involves altering the activity of OOM1 within a cell and then administering serine protease it to the cell. OOM1 bNA is useful for emarching serine protease in to the cell. OOM1 bNA is useful for generating non-human transgenic animal models, and for searching and identifying single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         population. OMM1 is useful as an immunogen to produce antibodies against COMM1 and in vitro assays to screen for agents or drugs, which modulate osteomalacia-related protein-1 (OOM-1).

Note: The present sequence states that this sequence is encoded by the DNA sequence shown in SEQ ID NO: 1 (AAD21889) of the specification. However this does not appear to be the case.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding a polypeptide useful for identifying polynucleotide expression or polypeptide activity modulators used for treating oncogenic osteomalacia, comprises the oncogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to oncogenic osteomalacia-related protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manavalan P, Levine MDM, Jan De Beur S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                        /note= "Bacterial extracellular solute-binding protein motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 82; DB 23; Length 525; 100.0%; Pred. No. 2.5e-05; ive 0; Mismatches 0; Indels (
                                                                                            442..455
/note= "Potential PKA phosphorylation site"
            264..275
/note= "Calcium binding motif"
                                                    ..424
te= "Calcium binding motif"
'note= "Cell attachment site"
                                                                                                                              477..481
/note= "Glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 2; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-2000; 2000US-191786P.
19-OCT-2000; 2000US-241598P.
                                                                                                                                                                                                                                                                                                                              22-MAR-2001; 2001WO-US09289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                            (GENZ ) GENZYME CORP. (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteomalacia-related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                          500..503
                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schiavi S, Madden S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-010720/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 AA;
                                                                                                                                                                                                                                                      WO200172826-A2
                                                                                              Modified-site
                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                            04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                      Domain
                                                        Domain
                                                                                                                                                                          Domain
```

Gowen LC, Hames LM;

```
ö
                                                         The present sequence is that of human osteoregulin mature polypeptide, i.e. lacking an N-terminal signal sequence.

Costeoregulin is a novel protein which plays a role in regulating both encostants, adiposity, and the calcification of atherosclerotic plaques. 2 Splice variants of human osteoregulin exe identified (see also AAB2021). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, animal cells and mammals with a targeted disruption of an animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with costeoregulin activity. The modulators of activity may be useful in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 82; DB 22; Length 540; 100.0%; Pred. No. 2.5e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB82921 standard; Protein; 556 AA.
Claim 1; Page 59-61; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 ERGDNDISPPSGDGQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB82921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXX
dxxx
```

RESULT 14 AAB82923

ò 셤

```
The present sequence is that of human osteoregulin, a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atheroscierotic plaques. The sequence is predicted from the nucleotide sequence (see AAH56809) of isolated osteoblast cDNA. A splice variant of human osteoregulin was also identified (see AAB25200). The invention provides novel costeoregulin proteins, nucleic acids which encode them, vectors, annimal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods to identify modulators of osteoregulin activity as useful as conferent mammals for diseases or disorders associated with the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification (claimed), for treating and preventing osteoporosis, and for stemation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin -
                                             Osteoregulin, human, bone, homeostasis, adipose, calcification, atherosclerosis, osteoporosis, osteopathic, antiarteriosclerotic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gowen LC, Hames LM;
                                                                                                                                                                                                                                            /note= "encoded by TCA"
                                                                                                                                                             1..37
/label= Signal_peptide
38..556
/label= Mature_protein
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 48-49; 90pp; English.
                                                                                                                                                                                                                                                                                                                                          27-FEB-2001; 2001EP-0301768.
                                                                                                                                                                                                                                                                                                                                                                       29-FEB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
                                                                                                                                                                                                                                                                                                                                                                                                                        (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-604111/69.
               Human osteoregulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH26809
                                                                                                                                                                                                                            Misc-difference
                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                           EP1130098-A2
                                                                                                                                                                                                                                                                                                           05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                             therapy.
                                                                                                                                                            Peptide
                                                                                                                                                                                            Protein
                                                                                                                                              Key
```

ö

Gapa

ö

Query Match 100.0%; Score 82; DB 22; Length 556; Best Local Similarity 100.0%; Pred. No. 2.6e-05; Matches 15; Conservative 0; Mismatches 0; Indels (

Search completed: January 29, 2004, 12:38:34 Job time : 28.0263 secs

277 ERGDNDISPFSGDGQ 291

g

ð

1 ERGDNDISPFSGDGQ 15

THIS PAGE BLANK (USPTO)

```
394
683
8299
11198
8299
1106
1106
1106
1107
1107
1257
2257
2257
2257
US-09-077-098A-7
\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}{\overset{\mathsf{n}}}}{\overset{\mathsf{n}}}}{\overset{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
   Sequence 7, Appli
Sequence 6, Appli
Sequence 21875, A
Sequence 6, Appli
Sequence 6, Appli
Sequence 12899, A
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 23, Appl
Sequence 213, Appl
Sequence 21, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5220, Ap
30321, A
55, Appli
2, Appli
23810, A
31126, A
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                   January 29, 2004, 12:37:19; Search time 11.4474 Seconds (without alignments) 55.442 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*

1: /cgn2 6/ptodata/1/iaa/5A COMB.pep:*

2: /cgn2 6/ptodata/1/iaa/5B COMB.pep:*

3: /cgn2 6/ptodata/1/iaa/5B COMB.pep:*

3: /cgn2 6/ptodata/1/iaa/6B COMB.pep:*

5: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*

5: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-077-098A-7
US-09-252-991A-21875
US-09-370-807-6
US-09-370-807-6
US-09-321-259-6
US-09-921-259-991A-21834
US-09-252-991A-21834
US-08-484-489-12
US-09-391-104-23
US-09-391-104-23
US-09-391-104-23
US-09-391-104-23
US-09-391-104-23
US-09-252-991A-26193
US-09-391A-26193
US-09-252-991A-26193
US-09-252-991A-30321
US-08-650-332-2
US-09-252-991A-30321
US-08-09-134-601C-5220
US-08-09-252-991A-30321
US-08-134-601C-5220
US-08-134-601C-5220
US-08-134-601C-5220
US-08-134-601C-5220
US-08-134-601C-5220
US-08-134-6126-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-252-991A-23810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -07-640-476-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-637-870-1
US-07-637-399-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-640-476-5
US-08-112-703-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                          1 ERGDNDISPFSGDGQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                           US-09-812-485A-47
82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .......
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.5
38.5
38.5
38.5
                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                                                                                                                    Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
```

```
APPLICANT: TOKUNAGA, Eiji
SAKAGUCHI, Masashi
MATSUO, Kazuo
HAMADA, Fukusaburo
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                 Sequence
Sequence
Sequence
Sequence
                                                                                                                                       Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                          Sequence
Sequence
Sequence
                                   Sequence
                                                                                                                                                                                                                                                                              Sequence
Sequence
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 624 Winth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
               US-08-054-077C-2
US-09-252-991A-27150
US-09-199-637A-405
US-09-104-406C-16
US-09-1013-977C-42
US-09-113-977C-42
US-09-351-048A-43
US-09-351-048A-43
US-09-351-048A-41
US-09-113-977C-41
US-09-113-977C-41
US-08-421-826A-10
US-08-424-826A-10
US-08-424-826A-10
US-08-426-828-694-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DAILAR

PILING DATE: 19-May-1998

PRIOR APPLICATION NUMBER: US/09/077,098A

APPLICATION NUMBER: PCT/DP97/03222

FILING DATE: 12-SEP-1997

APPLICATION NUMBER: JP 27,148/1996

FILING DATE: 19-SEP-1996

ATTORNEY AGENT INFORMATION:
NAME: KORNBAU, Anne M.

REGISTRATION NUMBER: 25,618

REGISTRATION NUMBER: 25,618

TELECOMMUNICATION INFORMATION:
TELEFAK: 202-737-3528

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTER/STICS:
                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2039 amino acida
TYPE: amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-077-098A-7
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09077098A Patent No. 6544519 GENERAL INFORMATION:
```

```
US-09-252-991A-21875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-370-807-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-921-259-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                           Gaps
                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Score 41; DB 4; Length 2039;
Pred. No. 4.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%; Score 41; DB 4; Length 2042; 80.0%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: PAR PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 25,618
REPERBNUE/COCKET UNMBER: TOKUNAGA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: JP 27,148/1996
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: KORNBAU, Anne M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,098A
FILING DATE: 19-May-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-077-098A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-252-991A-21875
; Sequence 21875, Application US/09252991A
; Parent No. 6551795
; GENERAL INPORMATION:
                                                                                                                                                                                                          Sequence 6, Application US/09077098A
Patent No. 6544519
GENERAL INFORMATION:
APPLICANT: TOKUNAGA, Eiji
SAKAGUCHI, Masashi
                                                                                                                                                                                                                                                                                                           MATSUO, Kazuo
HAMADA, Fukusaburo
TOKIYOSHI, Sachio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'YPE: amino acid
Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                              1599 bgbisPrscb 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1591 bgbiskrsgb 1600
                                                                           4 DNDISPFSGD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 DNDISPFSGD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                            US-09-077-098A-6
                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                               ò
```

```
Marc J. Rubenfield et al. VENTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO PSEUDOMONAS VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ACTOR 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 4; Length 302;
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
ITLE OF INVENTION: N-End Rule Pathway Enzymes
FILE REFERENCE: BB-1199
CURRENT APPLICATION NUMBER: US/09/370,807
CURRENT FILING DATE: 1999-08-09
BARLIER FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 3; 1
Pred. No. 2.2e+02;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
PILE OF INVENTION: N-End Rule Pathway Enzymes
FILE REFERENCE: BB-1199
                           AFFLICATION NUCLEIC ACID AND AMINO AC TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIC FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 21875
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/921,259
CURRENT FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/096,225
PRIOR FILING DATE: August 12, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09370807
Patent No. 6297034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09921259
Patent No. 6465234
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||| |:: |||:
137 QRGDIDVAILFGDGR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Office 97
SEQ ID NO 6
LENGTH: 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ERGDNDISPFSGDGO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 GDRELNPFSG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GDNDISPFSG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Zea mays
US-09-370-807-6
```

g

```
RESULT 8
US-08-704-711A-16
Sequence 16, Application US/08704711A
Sequence 16, Application US/08704711A
Sequence 16, Application US/08704711A
Sequence 16, Application US/08704711A
SERVED INVERTION
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: MATALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS;
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 1.05/08/704,711A FILING DATE: 20-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.0%; Score 38.5; DB 3; 64.3%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ACTION 435

CLASSIFICATION 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357

FILING DATE: 17-MAR-1995

PRIOR APPLICATION NUMBER: DE 443838.1

FILING DATE: 21-OCT-1994

APPLICATION NUMBER: DE 4409663.1

FILING DATE: 17-MAR-1994

ATTORNEY/AGENT INFORMATION:
NAMME: GRANADOO, PATTICLED D.

REGISTRATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 26083/124

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08448489; Patent No. 618402; CENERAL INFORMATION: APPLICANT: SEIKI, Motoharu; APPLICANT: SATO, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 RCDHRDNSPFDGPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RGDN-DISPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-448-489-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31834, Application US/09252991A

Sequence 31834, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: ARRUGINGS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31834

LENGTH: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERCHORNOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22899
LENGTH: 101
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.6%; Score 39; DB 4; Length 425; 53.3%; Pred. No. 1.6e+02; ive 2; Mismatches 5; Indels
                                                                                                                                                                                 Length 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 101;
                                                                                                                                                                                 Score 40; DB 4; I
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 4
Pred. No. 34;
2; Mismatches
                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22899, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.6%;
60.0%;
                                                                                                                                                                                 48.8%;
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
LENGTH: 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                427 GDRELNPFSG 436
                                                                                                                                                                                                                                                                         3 GDNDISPFSG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 DGELKPFSGD 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 DNDISPFSGD 13
                                                                                                             ; ORGANISM: Zea mays
US-09-921-259-6
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-252-991A-22899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-31834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-31834
```

à

```
a
                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
            TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 12
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL INFORMALION.
APPLICANT: WILL, HOYBE
HINZMANN, BETN
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Unknown Organism: Known Member of ; OTHER INFORMATION: Matrix Metalloproteinase Family US-08-448-489-12
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.0%; Score 38.5; DB 3; Length 469; Best Local Similarity 64.3%; Pred. No. 2.1e+02; Matches 9; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 2007-5109
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/704,711
FILING DATE: cUnknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09521220
Patent No. 6399348
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 469 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 RGDHRDNSPFDGPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RGDN-DISPFSGDG 14
APPLICANT: SHINAGAWA, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               904136
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-521-220-16
                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
US-09-252-991A-26193

US-09-252-991A-26193

Sequence 26193, Application US/09252991A

Sequence 26193, Application US/09252991A

Sequence 26193, Application US/09252991A

Sequence 26193, Application US-09252991A

Sequence 26193

GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

TITLE OF INVENTION: ABPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US/09/218

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26193

LENGTH: 169

"LENGTH: 169

"TOTAL OF THE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/09391104

patent No. 6399371

general No. 679370

general No. 679370
                                                                                                                                                                                                                                          Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                          Score 38.5; DB 4;
Pred. No. 2.1e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38.5; DB 4;
Pred. No. 2.1e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 4; Pred. No. 85; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NOS: 35
FastSEQ for Windows Version 3.0
; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-09-521-220-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.0%;
                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        th 46.3%;
Similarity 66.7%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 RGDHRDNSPFDGPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 RCDHRDNSPFDGPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RGDN-DISPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RGDN-DISPFSGDG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 64.5-
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-391-104-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 23
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-391-104-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
```

ઠે

```
ö
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VINCI, VICTOR A.
APPLICANT: CONDER, MICHAEL J.
APPLICANT: CONDER, MICHAEL J.
APPLICANT: MCDA, PHYLLIS C.
APPLICANT: MEDENES, CHARLES R.
APPLICANT: BANDRICKSON, LEE E.
APPLICANT: RAMBOSEK, JOHN
TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: P.O. BOX 2000; 126 E. LINCOLN AVENUE
CITY: RAHWAY
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                          Query Match 46.3%; Score 38; DB 1; Length 3038; Best Local Similarity 63.6%; Pred. No. 1.9e+03; Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PER PC compatible
COMPUTER: PER PC compatible
COMPUTER: PER PC compatible
COMPUTER: PER PC compatible
COMPUTER: PAPLICATION DATA:
APPLICATION NUMBER: US/08/637,640
FILING DATE: 23-AUG-1996
CLLASSIFICATION: DATA:
APPLICATION NUMBER: 08/148,132
FILING DATE: 01-NOV-1993
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INPERMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19076
TELECOMMUNICATION: INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 2;
Pred. No. 1.9e+03;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08637640
Patent No. 5849541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3038 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: TPKS Protein
US-08-637-640-2
                                                                                                         , ORGANISM: TPKS Protein US-08-450-332-2
                                                                                                                                                                                                                                                                                                                       878 ERGKNDLDSFS 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                            1 ERGDNDISPFS 11
                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
STRANDEDNESS:
                                                                   HYPOTHETICAL: Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UE
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-637-640-2
                                                                                                                                                                                                                                                                              ò
                                                                                                                                               Sequence 7324.703, Application US/09328352

Patent No. 6562958

GENERAL INPORMATION:

TOTALE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7703

LENGTH: 186

TYPE: PRT

TYPE: PRT

CORANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VINCI, VICTOR A.
APPLICANT: CONDER, MICHAEL J.
APPLICANT: MCADA, PHYLLIS C.
APPLICANT: MCADA, PHYLLIS C.
APPLICANT: REVES, CHRRISTOPHER D.
APPLICANT: HENDRICKSON, LEE E.
APPLICANT: RAMBOSEK, JOHN
TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 4; Length 186;
Pred. No. 94;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARES PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,332
FLING DATE: 25-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/POCKET UNMBER: 19076CA
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION: 10078CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-450-332-2
Sequence 2, Application US/08450332;
Patent No. 5744350;
GENERAL INFORMATION:
APPLICANT: VINCI, VICTOR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                          6 GGSDISPDSGAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GDNDISPFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 GETDVSPFS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 07065-0907
                                                                                                                                      US-09-328-352-7703
```

oy Op

Search completed: January 29, 2004, 12:41:37 Job time: 12.4474 secs